

SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
REGULATORY PROTEINS

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<151> 1999-06-25

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Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp			
35	40	45	
Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val			
50	55	60	
Pro His Ala Asp Gly Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly			
65	70	75	80
Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg			
85	90	95	
Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala			
100	105	110	
Pro Lys Ala Val Val His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr			
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Tyr Ile Ala Gly Pro Asn Lys Ser Trp Ala			
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 Val Glu Thr Gln Ala
 1 5
 ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163
 Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala
 10 15 20
 tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211
 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala
 25 30 35
 agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259
 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala
 40 45 50
 att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307
 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly
 55 60 65
 tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc 355

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Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
 70                               75                               80                               85

gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att      403
Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
                               90                               95                               100

ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg      451
Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
                               105                               110                               115

cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct      499
His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro
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Asn Lys Ser Trp Ala
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 20                               25                               30

Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp
 35                               40                               45

Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val
 50                               55                               60

Pro His Ala Asp Gly Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly
 65                               70                               75                               80

Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg
 85                               90                               95

Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala
 100                               105                               110

Pro Lys Ala Val Val His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr
 115                               120                               125

Tyr Ile Ala Gly Pro Asn Lys Ser Trp Ala
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<223> RXA00603

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                                         Met Lys Leu Asp Ser
                                         1 5
att gat cgc gca att att gcg gag ctt agc gcg aat gcg cgc atc tca 163
Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala Asn Ala Arg Ile Ser
                        10 15 20
aat ctc gca ctg gct gac aag gtg cat ctc act ccg gga cct tgc ttg 211
Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr Pro Gly Pro Cys Leu
                        25 30 35
agg agg gtg cag cgt ttg gaa gcc gaa gga atc att ttg ggc tac agc 259
Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile Ile Leu Gly Tyr Ser
                        40 45 50
gcg gac att cac cct gcg gtg atg aat cgt gga ttt gag gtg acc gtg 307
Ala Asp Ile His Pro Ala Val Met Asn Arg Gly Phe Glu Val Thr Val
                        55 60 65
gat gtc act ctc agc aac ttc gac cgc tcc act gta gac aat ttt gaa 355
Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr Val Asp Asn Phe Glu
                        70 75 80 85
agc tcc gtt gcg cag cat gat gaa gta ctg gag ttg cac agg ctt ttt 403
Ser Ser Val Ala Gln His Asp Glu Val Leu Glu Leu His Arg Leu Phe
                        90 95 100
ggt tcg cca gat tat ttt gtc cgc atc gcc gtt gct gat ttg gag gcg 451
Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val Ala Asp Leu Glu Ala
                        105 110 115
tat gag caa ttt tta tcc agt cac att caa acc gtg cca gga att gca 499
Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr Val Pro Gly Ile Ala
                        120 125 130
aag atc tca tca cgt ttt gct atg aaa gtg gtg aaa cca gct cgc ccc 547
Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val Lys Pro Ala Arg Pro
                        135 140 145
cag gtg tgaagcatgc attttgaagc atg 576
Gln Val
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<211> 151

<212> PRT

<213> Corynebacterium glutamicum

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Pro Gly Pro Cys Leu Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile		
35	40	45
Ile Leu Gly Tyr Ser Ala Asp Ile His Pro Ala Val Met Asn Arg Gly		
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Phe Glu Val Thr Val Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr		
65	70	75
Val Asp Asn Phe Glu Ser Ser Val Ala Gln His Asp Glu Val Leu Glu		
85	90	95
Leu His Arg Leu Phe Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val		
100	105	110
Ala Asp Leu Glu Ala Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr		
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Val Pro Gly Ile Ala Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val		
130	135	140
Lys Pro Ala Arg Pro Gln Val		
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<220>

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<223> RXN02946

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ccc	att	tgg	cca	gcc	gaa	ctc	ttc	gaa	gac	ctc	gac	cgc	aac	gga	cca	163
Pro	Ile	Trp	Pro	Ala	Glu	Leu	Phe	Glu	Asp	Leu	Asp	Arg	Asn	Gly	Pro	
				10					15					20		

atc	ccc	ctc	tac	ttc	caa	gta	gcc	caa	cgc	ctc	gaa	gac	ggc	atc	cgc	211
Ile	Pro	Leu	Tyr	Phe	Gln	Val	Ala	Gln	Arg	Leu	Glu	Asp	Gly	Ile	Arg	
			25					30					35			

agc	gga	gtc	ctc	cca	ccc	gga	gca	cgc	cta	gaa	aac	gag	atc	tcc	gtg	259
Ser	Gly	Val	Leu	Pro	Pro	Gly	Ala	Arg	Leu	Glu	Asn	Glu	Ile	Ser	Val	
		40					45					50				

gcg	aaa	cac	ctc	aac	gta	tcc	cgc	ccc	acc	gtc	cga	cgc	gcc	atc	caa	307
Ala	Lys	His	Leu	Asn	Val	Ser	Arg	Pro	Thr	Val	Arg	Arg	Ala	Ile	Gln	
	55					60					65					

gaa	gtc	gta	gac	aaa	ggc	ctc	tta	gtt	cgc	cgc	cgc	ggt	gtt	ggc	acc	355
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Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg Arg Gly Val Gly Thr
 70 75 80 85
 cag gtc gtc caa agc cac gtc acc cgc cca gtc gaa ctg acc agt ttc 403
 Gln Val Val Gln Ser His Val Thr Arg Pro Val Glu Leu Thr Ser Phe
 90 95 100
 ttc aac gac ctc aaa aac gcc aac ctg gac ccc aaa acc cga gtc ctc 451
 Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro Lys Thr Arg Val Leu
 105 110 115
 gag cac cgc tcc ttg cag caa gtt ccg cca tcg cag aaa aac tcg gag 499
 Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser Gln Lys Asn Ser Glu
 120 125 130
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 Phe Pro Gln Val Thr Lys Ser Ser Ser Ser Ala Ala Ser Ala Pro Pro
 135 140 145
 gag aca tcc ccg tagcgatcct ggaaaactac ctc 582
 Glu Thr Ser Pro
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 35 40 45
 Asn Glu Ile Ser Val Ala Lys His Leu Asn Val Ser Arg Pro Thr Val
 50 55 60
 Arg Arg Ala Ile Gln Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg
 65 70 75 80
 Arg Gly Val Gly Thr Gln Val Val Gln Ser His Val Thr Arg Pro Val
 85 90 95
 Glu Leu Thr Ser Phe Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro
 100 105 110
 Lys Thr Arg Val Leu Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser
 115 120 125
 Gln Lys Asn Ser Glu Phe Pro Gln Val Thr Lys Ser Ser Ser Ser Ala
 130 135 140
 Ala Ser Ala Pro Pro Glu Thr Ser Pro
 145 150

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Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala	50	55	60
Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly	65	70	75
Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr	85	90	95
Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly	100	105	110
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Leu Ala Asp Leu Val Ala Gly Leu	130	135	

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 Val Glu Ile Arg Trp
 1 5
 ttg gaa ggc ttt atc gcg gtc gcg gaa gaa ttg cac ttt agt aat gct 163
 Leu Glu Gly Phe Ile Ala Val Ala Glu Glu Leu His Phe Ser Asn Ala
 10 15 20
 gcg att cgt ttg ggg atg ccg caa tcg ccg ttg agt cag ttg atc cgg 211
 Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu Ser Gln Leu Ile Arg
 25 30 35
 cgg ttg gag tcg gag ttg ggg cag aag ctt ttt gat cgc agt acc cgg 259
 Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe Asp Arg Ser Thr Arg
 40 45 50
 tcg gtg gag tta act gcc gcg ggt cgg gcg ttt ttg cca cat gcc agg 307
 Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe Leu Pro His Ala Arg
 55 60 65
 ggg att gtg gcg agc gct gcg gtg gcg agg gaa gct gtg aat gct gcc 355

Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu Ala Val Asn Ala Ala
 70 75 80 85
 gag ggg gag atc gtt ggt gtt gtt cgc att ggt ttt tct ggt gtg ctg 403
 Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly Phe Ser Gly Val Leu
 90 95 100
 aac tat tcc acg ctg ccg ctt ttg acc agt gag gtg cat aaa cgg ctt 451
 Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu Val His Lys Arg Leu
 105 110 115
 cct aat gtg gag ttg gag ctg gtt ggt cag aag ttg acg agg gaa gcg 499
 Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys Leu Thr Arg Glu Ala
 120 125 130
 gta agt ttg ctg cgc ttg ggg gcg ttg gat att acg ttg atg ggt ttg 547
 Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile Thr Leu Met Gly Leu
 135 140 145
 ccc att gag gat cca gag att gag act cgg ctg att agt ttg gaa gag 595
 Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu Ile Ser Leu Glu Glu
 150 155 160 165
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 Phe Cys Val Val Leu Pro Lys Asp His Arg Leu Ala Gly Glu Gly Val
 170 175 180
 gtg gat ttg gtg gat ctg gct aaa gat ggg ttt gtg acg acg ccg gag 691
 Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe Val Thr Thr Pro Glu
 185 190 195
 ttt gcg ggg tct gtg ttt agg aat tcc acc ttt cag ttg tgt gct gag 739
 Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe Gln Leu Cys Ala Glu
 200 205 210
 gct ggt ttt gtg ccg agg atc agc cag caa gtt aat gat cct tac atg 787
 Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val Asn Asp Pro Tyr Met
 215 220 225
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<213> Corynebacterium glutamicum

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 35 40 45

Asp Arg Ser Thr Arg Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe
 50 55 60

Leu Pro His Ala Arg Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu
 65 70 75 80
 Ala Val Asn Ala Ala Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly
 85 90 95
 Phe Ser Gly Val Leu Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu
 100 105 110
 Val His Lys Arg Leu Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys
 115 120 125
 Leu Thr Arg Glu Ala Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile
 130 135 140
 Thr Leu Met Gly Leu Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu
 145 150 155 160
 Ile Ser Leu Glu Glu Phe Cys Val Val Leu Pro Lys Asp His Arg Leu
 165 170 175
 Ala Gly Glu Gly Val Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe
 180 185 190
 Val Thr Thr Pro Glu Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe
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 225 230 235

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 <223> RXN02553

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 Met Ala Val Lys Arg
 1 5
 aat gag ttg gaa ccc gag ctg acg tcc aac ccc aac cca tta agc gca 163
 Asn Glu Leu Glu Pro Glu Leu Thr Ser Asn Pro Asn Pro Leu Ser Ala
 10 15 20
 gaa gtg cat cat ttg tat cct gag gaa act cgt ctt gca acg gag atc 211
 Glu Val His His Leu Tyr Pro Glu Glu Thr Arg Leu Ala Thr Glu Ile
 25 30 35
 ctg gaa cgc acc aac aat tgg ctt gct gaa aaa ggg atc cct ccg ctg 259

Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys Gly Ile Pro Pro Leu
 40 45 50

cca cca gcg gaa gtt gta gcc atc tca tta cac ctg gtt aat gct ggt 307
 Pro Pro Ala Glu Val Val Ala Ile Ser Leu His Leu Val Asn Ala Gly
 55 60 65

ttc cgc acg gaa gac ctc gca gaa acc tac gtg atg act ggc gtt ttc 355
 Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val Met Thr Gly Val Phe
 70 75 80 85

gag cag ctc ttt gag gta atc gat tcc tcg ttt ggc atc acc ctt gac 403
 Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe Gly Ile Thr Leu Asp
 90 95 100

cga caa tcc gtc aac gcc gca cgg ttt atc acc cac atg cgc tac ttc 451
 Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr His Met Arg Tyr Phe
 105 110 115

ttt gtt cgc gtt cac cac gac gga caa ctc aac gac ggc atg tcc gtg 499
 Phe Val Arg Val His His Asp Gly Gln Leu Asn Asp Gly Met Ser Val
 120 125 130

ctg cgc aac agc cta gaa att tcc cac ccg gat tcg gtg gca tgt gcg 547
 Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp Ser Val Ala Cys Ala
 135 140 145

gaa aga ctc agc caa atc ctc agc ctt cga ttg ggt gcc gaa ctt tcc 595
 Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu Gly Ala Glu Leu Ser
 150 155 160 165

tcc gac gag caa acc tac ctc gcg ctc cat gtc gcg agg ttg gct gaa 643
 Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val Ala Arg Leu Ala Glu
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 185

<210> 14

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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Asn Pro Leu Ser Ala Glu Val His His Leu Tyr Pro Glu Glu Thr Arg
 20 25 30

Leu Ala Thr Glu Ile Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys
 35 40 45

Gly Ile Pro Pro Leu Pro Pro Ala Glu Val Val Ala Ile Ser Leu His
 50 55 60

Leu Val Asn Ala Gly Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val
 65 70 75 80

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Met Ala Gly Gly Asn															
1 5															
cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga															163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly															
10 15 20															
gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag															211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu															
25 30 35															
ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta															259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu															
40 45 50															
acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg															307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu															
55 60 65															
ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc															355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg															
70 75 80 85															
gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag															403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu															

	90	95	100	
act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac				451
Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp				
	105	110	115	
cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt				499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly				
	120	125	130	
cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt				547
Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe				
	135	140	145	
gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc				595
Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala				
	150	155	160	165
tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg				643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu				
	170	175	180	
aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga				691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg				
	185	190	195	
atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg				739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu				
	200	205	210	
gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt				787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu				
	215	220	225	
gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa				835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys				
	230	235	240	245
gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat				883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn				
	250	255	260	
gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata				927
Ala Glu Arg Lys Gly Asp Thr				
	265			

<210> 16

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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1				5				10						15	

Ile	Ala	Val	Leu	Gly	Ala	Phe	Glu	His	Thr	Met	Arg	Pro	Leu	Gly	Val
		20						25					30		

Thr	Glu	Ile	Ala	Glu	Leu	Ala	Asp	Leu	Pro	Pro	Ser	Thr	Thr	His	Arg
		35					40					45			

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
 50 55 60
 Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
 65 70 75 80
 Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95
 Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110
 Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125
 Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140
 Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
 145 150 155 160
 Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175
 Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190
 His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205
 His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220
 Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240
 Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
 245 250 255
 Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
 260 265

<210> 17
 <211> 777
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(754)
 <223> RXS00774

<400> 17
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 acacaatcta atcattttgt gtgatctaac taaggagtgc atg gat aag gcg act 115
 Met Asp Lys Ala Thr
 1 5

gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc 163
Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
10 15 20

aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
25 30 35

gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
40 45 50

gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
55 60 65

ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg 355
Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
70 75 80 85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
90 95 100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
105 110 115

cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
120 125 130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac 547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
135 140 145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag 595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
150 155 160 165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg 643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
170 175 180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
185 190 195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
200 205 210

ttc cgc acc agc gag taaaaagctg cttctcgacg cta 777
Phe Arg Thr Ser Glu
215

<210> 18

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

Met Asp Lys Ala Thr Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala
 1 5 10 15

Glu Ser Ala Leu Gly Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly
 20 25 30

Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala
 35 40 45

Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
 50 55 60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
 65 70 75 80

Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
 85 90 95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
 100 105 110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
 115 120 125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
 130 135 140

Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
 145 150 155 160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
 165 170 175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
 180 185 190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
 195 200 205

Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
 210 215

<210> 19

<211> 1362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1339)

<223> RXN02493

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gcagcagtag caaacagg taataagtag ctatttgtag gtg agc act ctt ctt 115
 Val Ser Thr Leu Leu
 1 5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat	163
Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr	
10 15 20	
acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg	211
Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu	
25 30 35	
tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att	259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile	
40 45 50	
caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc	307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val	
55 60 65	
atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga	355
Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg	
70 75 80 85	
tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac	403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp	
90 95 100	
caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc	451
Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg	
105 110 115	
ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg	499
Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr	
120 125 130	
ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa	547
Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu	
135 140 145	
aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc	595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser	
150 155 160 165	
cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc	643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
170 175 180	
ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc	691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser	
185 190 195	
agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg	739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu	
200 205 210	
atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa	787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu	
215 220 225	
ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa	835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln	
230 235 240 245	

ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc 883
 Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr
 250 255 260

ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg 931
 Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala
 265 270 275

aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc 979
 Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val
 280 285 290

tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc 1027
 Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr
 295 300 305

gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa 1075
 Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu
 310 315 320 325

aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act 1123
 Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr
 330 335 340

ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt 1171
 Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly
 345 350 355

agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt 1219
 Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu
 360 365 370

gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag 1267
 Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys
 375 380 385

cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca 1315
 Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala
 390 395 400 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgatcggt gaa 1362
 Ser Gly Arg Arg Lys Glu Lys Ser
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<210> 20

<211> 413

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu
 1 5 10 15

Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys
 20 25 30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val
 35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp

50	55	60
Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly 65 70 75 80		
Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln 85 90 95		
Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp 100 105 110		
Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val 115 120 125		
Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala 130 135 140		
Ser Asp Glu Ser Glu Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe 145 150 155 160		
Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala 165 170 175		
Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val 180 185 190		
Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp 195 200 205		
Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg 210 215 220		
Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala 225 230 235 240		
Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile 245 250 255		
Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu 260 265 270		
Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro 275 280 285		
Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val 290 295 300		
Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln 305 310 315 320		
Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg 325 330 335		
Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met 340 345 350		
Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly 355 360 365		
Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu 370 375 380		

Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr
 385 390 395 400

Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser
 405 410

<210> 21
 <211> 1362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1339)
 <223> FRXA02493

<400> 21
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gcagcagtag caaaccaggg taataagtag ctattttagtag gtg agc act ctt ctt 115
 Val Ser Thr Leu Leu
 1 5

gct ttc gta ttg ggc gtg gtc ctc atg ggc ctc gcc cta cct gcg tat 163
 Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr
 10 15 20

acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg 211
 Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu
 25 30 35

tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att 259
 Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile
 40 45 50

caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc 307
 Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val
 55 60 65

atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga 355
 Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg
 70 75 80 85

tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac 403
 Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp
 90 95 100

caa gaa acc cac tca ctc gac gtc cac cca gac cgc aat ccg cgg cgc 451
 Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg
 105 110 115

ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg 499
 Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr
 120 125 130

ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa 547
 Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu
 135 140 145

aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc	595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser	
150 155 160 165	
cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc	643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
170 175 180	
ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc	691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser	
185 190 195	
agg ctc cac cgc gaa gcc cac cgc atg gcc gac atg atc aac gaa ctg	739
Arg Leu His Arg Glu Ala His Arg Met Ala Asp Met Ile Asn Glu Leu	
200 205 210	
atc tcc ctt tcc aaa ctt cag ggc gcc gaa cga ctc cct gat atg gaa	787
Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu	
215 220 225	
ccc gtc cag gct gac gac atc atc agc gaa gcc atc gaa cgc acc caa	835
Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln	
230 235 240 245	
ctc gcc gcc gac aac gcc aac atc gaa atc att cgc ggc gac cgc acc	883
Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr	
250 255 260	
ggc gtt tgg gta gaa gcc gat cga tcc ctg ctg gtc aca gcc ctg gcg	931
Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu Val Thr Ala Leu Ala	
265 270 275	
aac ctg atc agc aat gca atc aac tac tca cca aaa tca gtc ccc gtc	979
Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro Lys Ser Val Pro Val	
280 285 290	
tcc gtt tca caa agc atc cga aac gac gtg gtc atg atc cga gta acc	1027
Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val Met Ile Arg Val Thr	
295 300 305	
gac cgt ggc att ggc atc gca ccc gaa gac caa ggc cga gtt ttc gaa	1075
Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln Gly Arg Val Phe Glu	
310 315 320 325	
aga ttc ttc cgc gtc gac aaa gcc cgc tcc cgc caa acc ggc gga act	1123
Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg Gln Thr Gly Gly Thr	
330 335 340	
ggc ctt ggc ctc gcg ata gtc aaa cat gtc atg gct aac cat ggc ggt	1171
Gly Leu Gly Leu Ala Ile Val Lys His Val Met Ala Asn His Gly Gly	
345 350 355	
agt att agt ttg tgg tca cgt cct gga aca ggc tcc aca ttt aca ctt	1219
Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly Ser Thr Phe Thr Leu	
360 365 370	
gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag	1267
Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys	
375 380 385	
cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca	1315

Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala
 390 395 400 405

tct ggg cgc cga aag gaa aaa tca tgacgagaat cctgacggtt gaa 1362
 Ser Gly Arg Arg Lys Glu Lys Ser
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<210> 22

<211> 413

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Val Ser Thr Leu Leu Ala Phe Val Leu Gly Val Val Leu Met Gly Leu
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Ala Leu Pro Ala Tyr Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys
 20 25 30

Ser Ala Val Thr Leu Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val
 35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp
 50 55 60

Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly
 65 70 75 80

Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln
 85 90 95

Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp
 100 105 110

Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val
 115 120 125

Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala
 130 135 140

Ser Asp Glu Ser Glu Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe
 145 150 155 160

Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
 165 170 175

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
 180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
 195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
 210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
 225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile
 245 250 255

Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu
 260 265 270
 Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro
 275 280 285
 Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
 290 295 300
 Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln
 305 310 315 320
 Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg
 325 330 335
 Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met
 340 345 350
 Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly
 355 360 365
 Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu
 370 375 380
 Pro Ala Gly Ser Lys Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr
 385 390 395 400
 Thr Ala Ser Lys Ala Ser Gly Arg Arg Lys Glu Lys Ser
 405 410

<210> 23
 <211> 1578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1555)
 <223> RXN00631

<400> 23
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 ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat 115
 Met Glu Asn Pro Tyr
 1 5
 gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa 163
 Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
 10 15 20
 gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc 211
 Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
 25 30 35
 ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg 259
 Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
 40 45 50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa	307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu	
55 60 65	
ggt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg	355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr	
70 75 80 85	
tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg	403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly	
90 95 100	
cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc	451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser	
105 110 115	
atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc	499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr	
120 125 130	
atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc	547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser	
135 140 145	
aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc	595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr	
150 155 160 165	
gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg	643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu	
170 175 180	
gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg	691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu	
185 190 195	
att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa	739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu	
200 205 210	
ggt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt	787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg	
215 220 225	
gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc	835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala	
230 235 240 245	
ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag	883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln	
250 255 260	
caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag	931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu	
265 270 275	
ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca	979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser	
280 285 290	
tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc	1027

Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
 295 300 305
 gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg 1075
 Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
 310 315 320 325
 cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa 1123
 Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
 330 335 340
 ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc 1171
 Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
 345 350 355
 aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc 1219
 Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
 360 365 370
 gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga 1267
 Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
 375 380 385
 cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc 1315
 Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
 390 395 400 405
 gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363
 Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
 410 415 420
 tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411
 Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
 425 430 435
 tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc 1459
 Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
 440 445 450
 acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507
 Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
 455 460 465
 gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct 1555
 Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
 470 475 480 485
 taaaggcatc aagggccgga aaa 1578

<210> 24

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val
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Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
 20 25 30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
 35 40 45
 Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
 50 55 60
 Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
 65 70 75 80
 Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
 85 90 95
 Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
 100 105 110
 Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
 115 120 125
 Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
 130 135 140
 Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
 145 150 155 160
 Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
 165 170 175
 Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
 180 185 190
 Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
 195 200 205
 Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
 210 215 220
 Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
 225 230 235 240
 Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
 245 250 255
 Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
 260 265 270
 Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe
 275 280 285
 Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
 290 295 300
 Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
 305 310 315 320
 Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg
 325 330 335
 Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
 340 345 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
 355 360 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
 370 375 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
 385 390 395 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
 405 410 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
 420 425 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
 435 440 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
 450 455 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
 465 470 475 480

Leu Pro Ala Val Ser
 485

<210> 25
 <211> 1606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (12)..(1583)
 <223> RXN00291

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 Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly
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att ttc gca gtt ttg atg atg gat cag atg aaa act gag gcc gag cac 98
 Ile Phe Ala Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His
 15 20 25

aca gcg ctg tcc atc gga cgt tgg gtg gca tcc aac ccg cag atc cgc 146
 Thr Ala Leu Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg
 30 35 40 45

gag gaa gta gcg ctt gat act caa aca gga gca aac cca tcg gcc gaa 194
 Glu Glu Val Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu
 50 55 60

gaa tta gcc gat gga gat atc caa gcg gtt gca cag gcg gcc aat gaa 242
 Glu Leu Ala Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu
 65 70 75

cgc act gga gct ttg ttt gtc gtt atc act gac ggt tta ggt atc cgc 290
 Arg Thr Gly Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg

80	85	90	
ctg tcc cac cca gat gag gaa cgt ctg ggg gag cag gtg agc act agc Leu Ser His Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser 95 100 105			338
ttt gag gct gcc atg cgg ggt gaa gaa acc atg gcg tgg gag act ggg Phe Glu Ala Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly 110 115 120 125			386
acc ctc ggt gcg tcc gcg cga gca aaa gtg cct atc ttt gcg ccg gat Thr Leu Gly Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp 130 135 140			434
tct agt gtt cca gtc ggt gag gtc agt gtt ggg ttt gag cga gac agt Ser Ser Val Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser 145 150 155			482
gtg tat tcc cgc ctg ccc atg ttc ctc gcc gcc ctt gct ctt att tct Val Tyr Ser Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser 160 165 170			530
gtg ttg gga atc ctt atc ggc gtg ggt gta gcc atg ggc atg cga cgc Val Leu Gly Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg 175 180 185			578
cgt tgg gaa cgc gtg acc ttg ggt ttg cag ccg gag gag cta gtg acc Arg Trp Glu Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr 190 195 200 205			626
ctt gtg caa aat cag act gca gtc atc gat ggc att gat gag ggc gtg Leu Val Gln Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val 210 215 220			674
ctg gcg ctg agc cca aac gga aca att ggg gtg cat aat gag cag gcg Leu Ala Leu Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala 225 230 235			722
caa tcc atg att ggt gca ggt cct atg agt ggc agg acg ttg aaa gaa Gln Ser Met Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu 240 245 250			770
cta ggg ctt gac ctg ggt ctt gat ggc gtt gta ttg cat ggt cag cat Leu Gly Leu Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His 255 260 265			818
ccg gaa acc gtt gcc cat aac ggc agg atc ctc tat ctg gat ttc cac Pro Glu Thr Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His 270 275 280 285			866
ccc gtg cgc cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc Pro Val Arg Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg 290 295 300			914
gat cgt acc gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc Asp Arg Thr Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg 305 310 315			962
acc atg acc cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc Thr Met Thr His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg 320 325 330			1010

atc cac acc gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg 1058
 Ile His Thr Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala
 335 340 345
 gca gag ttt cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca 1106
 Ala Glu Phe Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro
 350 355 360 365
 ttg atc gga tca gcg cac ctc aat gaa gca ttt ttg agc tca ttt tta 1154
 Leu Ile Gly Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu
 370 375 380
 agt act gct tct att tcg gca tct gaa aag ggc gtt agt ctg cgc atc 1202
 Ser Thr Ala Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile
 385 390 395
 aac tct gac acg ctc atc ctt ggc act gtt aaa gat cca gaa gat gta 1250
 Asn Ser Asp Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val
 400 405 410
 gca acc att ttg ggt aat tta atc aac aat gcc atc gac gcc gcg gtg 1298
 Ala Thr Ile Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val
 415 420 425
 gca ggt gaa gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc 1346
 Ala Gly Glu Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala
 430 435 440 445
 gat acg ctg gtc att tct gtt gca gat tct ggt cct gga atc cca gag 1394
 Asp Thr Leu Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu
 450 455 460
 ggc gtg gat gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat 1442
 Gly Val Asp Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp
 465 470 475
 aat gaa cgc acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct 1490
 Asn Glu Arg Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala
 480 485 490
 ttg gct aga tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc 1538
 Leu Ala Arg Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr
 495 500 505
 gaa gat ggc gct gta ttt gga gtg aaa cta ccg gga gta atg gag 1583
 Glu Asp Gly Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu
 510 515 520
 taatggatca aacacttaaa gtt 1606

<210> 26

<211> 524

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly Ile Phe Ala
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Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His Thr Ala Leu
 20 25 30
 Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val
 35 40 45
 Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala
 50 55 60
 Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly
 65 70 75 80
 Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His
 85 90 95
 Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala
 100 105 110
 Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly
 115 120 125
 Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val
 130 135 140
 Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser
 145 150 155 160
 Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly
 165 170 175
 Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu
 180 185 190
 Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln
 195 200 205
 Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu
 210 215 220
 Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met
 225 230 235 240
 Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu
 245 250 255
 Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr
 260 265 270
 Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg
 275 280 285
 Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr
 290 295 300
 Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr
 305 310 315 320
 His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg Ile His Thr
 325 330 335
 Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe

340					345					350					
Leu	Gly	Asp	Ile	Ser	Arg	Asn	Gly	Gly	Gln	Ser	His	Pro	Leu	Ile	Gly
		355					360					365			
Ser	Ala	His	Leu	Asn	Glu	Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala
		370					375					380			
Ser	Ile	Ser	Ala	Ser	Glu	Lys	Gly	Val	Ser	Leu	Arg	Ile	Asn	Ser	Asp
		385				390				395					400
Thr	Leu	Ile	Leu	Gly	Thr	Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile
				405					410					415	
Leu	Gly	Asn	Leu	Ile	Asn	Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu
			420					425						430	
Ala	Pro	Arg	Trp	Ile	Glu	Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu
			435				440					445			
Val	Ile	Ser	Val	Ala	Asp	Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp
			450			455					460				
Val	Phe	Ala	Thr	Ala	Thr	Gln	Ile	Gly	Asp	Ser	Glu	Asp	Asn	Glu	Arg
					470					475					480
Thr	His	Gly	His	Gly	Ile	Gly	Leu	Lys	Leu	Cys	Arg	Ala	Leu	Ala	Arg
				485					490					495	
Ser	His	Gly	Gly	Asp	Val	Trp	Val	Ile	Asp	Arg	Gly	Thr	Glu	Asp	Gly
			500					505					510		
Ala	Val	Phe	Gly	Val	Lys	Leu	Pro	Gly	Val	Met	Glu				
			515				520								

<210> 27
 <211> 1097
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1074)
 <223> FRXA00291

<400> 27																
gcc	gcc	ctt	gct	ctt	att	tct	gtg	ttg	gga	atc	ctt	atc	ggc	gtg	ggt	48
Ala	Ala	Leu	Ala	Leu	Ile	Ser	Val	Leu	Gly	Ile	Leu	Ile	Gly	Val	Gly	
1				5				10					15			
gta gcc atg ggc atg cga cgc cgt tgg gaa cgc gtg acc ttg ggt ttg															96	
Val	Ala	Met	Gly	Met	Arg	Arg	Arg	Trp	Glu	Arg	Val	Thr	Leu	Gly	Leu	
			20					25					30			
cag ccg gag gag cta gtg acc ctt gtg caa aat cag act gca gtc atc															144	
Gln	Pro	Glu	Glu	Leu	Val	Thr	Leu	Val	Gln	Asn	Gln	Thr	Ala	Val	Ile	
			35				40					45				
gat ggc att gat gag ggc gtg ctg gcg ctg agc cca aac gga aca att															192	
Asp	Gly	Ile	Asp	Glu	Gly	Val	Leu	Ala	Leu	Ser	Pro	Asn	Gly	Thr	Ile	

50	55	60	
ggg gtg cat aat gag cag gcg caa tcc atg att ggt gca ggt cct atg			240
Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met			
65	70	75	80
agt ggc agg acg ttg aaa gaa cta ggg ctt gac ctg ggt ctt gat ggc			288
Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly			
	85	90	95
gtt gta ttg cat ggt cag cat ccg gaa acc gtt gcc cat aac ggc agg			336
Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg			
	100	105	110
atc ctc tat ctg gat ttc cac ccc gtg cgc cgt ggg gat caa gat tta			384
Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu			
	115	120	125
ggc tac gtg gta acc atc cgc gat cgt acc gac atc att gaa ctc agt			432
Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser			
	130	135	140
gaa cgc ctc gac tct gtg cgc acc atg acc cac gca ctc cgc gcc cag			480
Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln			
	145	150	155
cgc cac gag ttt gcc aac cgc atc cac acc gca aca ggg ctt atc gac			528
Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp			
	165	170	175
gcc ggc cgc gtc cac gac gcg gca gag ttt cta ggc gat ata tcc cgc			576
Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg			
	180	185	190
aac ggg gga cag tca cat cca ttg atc gga tca gcg cac ctc aat gaa			624
Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu			
	195	200	205
gca ttt ttg agc tca ttt tta agt act gct tct att tcg gca tct gaa			672
Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser Glu			
	210	215	220
aag ggc gtt agt ctg cgc atc aac tct gac acg ctc atc ctt ggc act			720
Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly Thr			
	225	230	235
gtt aaa gat cca gaa gat gta gca acc att ttg ggt aat tta atc aac			768
Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile Asn			
	245	250	255
aat gcc atc gac gcc gcg gtg gca ggt gaa gcc cca cgg tgg att gag			816
Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu			
	260	265	270
ctt acg ttg atg gat gat gcc gat acg ctg gtc att tct gtt gca gat			864
Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp			
	275	280	285
tct ggt cct gga atc cca gag ggc gtg gat gta ttt gcc aca gcc acc			912
Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr			
	290	295	300

cag ata gga gac tct gaa gat aat gaa cgc acc cac ggg cat ggc att 960
 Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
 305 310 315 320
 ggt cta aaa ctg tgc cgg gct ttg gct aga tca cat ggt ggc gat gtc 1008
 Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
 325 330 335
 tgg gtg att gat aga gga acc gaa gat ggc gct gta ttt gga gtg aaa 1056
 Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys
 340 345 350
 cta ccg gga gta atg gag taatggatca aacacttaaa gtt 1097
 Leu Pro Gly Val Met Glu
 355

<210> 28
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
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 Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly Leu
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 Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val Ile
 35 40 45
 Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile
 50 55 60
 Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met
 65 70 75 80
 Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly
 85 90 95
 Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg
 100 105 110
 Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu
 115 120 125
 Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser
 130 135 140
 Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln
 145 150 155 160
 Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp
 165 170 175
 Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg
 180 185 190
 Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu

195					200					205					
Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala	Ser	Ile	Ser	Ala	Ser	Glu
210						215					220				
Lys	Gly	Val	Ser	Leu	Arg	Ile	Asn	Ser	Asp	Thr	Leu	Ile	Leu	Gly	Thr
225					230					235					240
Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile	Leu	Gly	Asn	Leu	Ile	Asn
				245					250					255	
Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu	Ala	Pro	Arg	Trp	Ile	Glu
			260					265					270		
Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu	Val	Ile	Ser	Val	Ala	Asp
		275					280					285			
Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp	Val	Phe	Ala	Thr	Ala	Thr
	290					295					300				
Gln	Ile	Gly	Asp	Ser	Glu	Asp	Asn	Glu	Arg	Thr	His	Gly	His	Gly	Ile
305					310					315					320
Gly	Leu	Lys	Leu	Cys	Arg	Ala	Leu	Ala	Arg	Ser	His	Gly	Gly	Asp	Val
				325					330					335	
Trp	Val	Ile	Asp	Arg	Gly	Thr	Glu	Asp	Gly	Ala	Val	Phe	Gly	Val	Lys
			340					345					350		
Leu	Pro	Gly	Val	Met	Glu										
		355													

<210> 29
 <211> 1620
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1597)
 <223> RXA00129

<400> 29
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 tcgcattgta gataaatggc gaacctcact gcaggttcgc gtg ctc ggc tcc atc 115
 Val Leu Gly Ser Ile
 1 5
 ttc acc gca tca gct gtc gtg atg atc ctt ttg ggg ctg ggc atg ctg 163
 Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu Gly Leu Gly Met Leu
 10 15 20
 act gta ttc acc caa cgg ttg gtg gat cag aaa atc gat att gcg agc 211
 Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys Ile Asp Ile Ala Ser
 25 30 35
 tcc gaa atc gac cgc gcc cgc gtc atc gtc gaa gag caa atc acc gca 259
 Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu Glu Gln Ile Thr Ala
 40 45 50

tcc ggc gcc tca aca tcg gtg cag gcg cga gtg aac tct gcc cgc gct	307
Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val Asn Ser Ala Arg Ala	
55 60 65	
gcg ctc tcc agc ttg ggt acc agc ggc ggt aca gaa acc aac gcc gcc	355
Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr Glu Thr Asn Ala Ala	
70 75 80 85	
tac gat cca gtc gtg ttg gtg aac aac gat gac ctg gtg gtc tct ccc	403
Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp Leu Val Val Ser Pro	
90 95 100	
gag ggt tac caa atc cca gaa cgt ctg cga tac ttc gtc tct gag aac	451
Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr Phe Val Ser Glu Asn	
105 110 115	
caa gtc tcg tat cag ttc tcc agc atc gac caa ggc gac gga tcg tcc	499
Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln Gly Asp Gly Ser Ser	
120 125 130	
tac caa gcg ctc atc atc gga acg ccc acg gaa agc gac atc ccg aac	547
Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu Ser Asp Ile Pro Asn	
135 140 145	
ctc cag gtg tat ctg gtg ttc tcc atg gaa agc gac gaa tcc tct ctt	595
Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser Asp Glu Ser Ser Leu	
150 155 160 165	
gct ctc atg cga gga ctc ctc tca gct gca ctg ctg atc gtg gtg gtg	643
Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu Leu Ile Val Val Val	
170 175 180	
ctg ctg gtc ggt atc gca tgg cta gcc acc caa cag gtc acc gcg ccg	691
Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln Gln Val Thr Ala Pro	
185 190 195	
gtg cgt tcg gcg agc cgg att gcg gag cgt ttc gct caa ggc aaa ctg	739
Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe Ala Gln Gly Lys Leu	
200 205 210	
cgt gaa cgc atg gtg gtg gaa ggc gaa gac gag atg gcc cgc ctg gcg	787
Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu Met Ala Arg Leu Ala	
215 220 225	
gtg tcc ttc aac gcg atg gcc gaa tcg ctg tcc gcg cag atc acc aaa	835
Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser Ala Gln Ile Thr Lys	
230 235 240 245	
ttg gag gaa tac ggc aat ctg caa cga caa ttc aca tcg gat gtc tca	883
Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe Thr Ser Asp Val Ser	
250 255 260	
cac gaa ttg cgc aca ccg ctg aca acg gtg cgc atg gct gct gat cta	931
His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg Met Ala Ala Asp Leu	
265 270 275	
att gcc gat agt gaa gat gaa ctt tca ccc ggt gcg cgc cgc gcc agc	979
Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly Ala Arg Arg Ala Ser	
280 285 290	

caa ctg atg aac agg gag ttg gac cga ttc gag tcg ctg ctg agc gat	1027
Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu Ser Leu Leu Ser Asp	
295 300 305	
ctg ttg gaa att tcc cga cac gac gcc ggc gtt gcc gaa ctg tcc acc	1075
Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val Ala Glu Leu Ser Thr	
310 315 320 325	
gcg ctt cac gat gtc cgc atc cca gtg cga tcg gca ttg gaa caa gta	1123
Ala Leu His Asp Val Arg Ile Pro Val Arg Ser Ala Leu Glu Gln Val	
330 335 340	
caa cac ttg gcc acc gag ctc gat gtg gaa ttg ctt gtt aat ttg ccc	1171
Gln His Leu Ala Thr Glu Leu Asp Val Glu Leu Leu Val Asn Leu Pro	
345 350 355	
gaa gaa gcg atc aac att caa ggc gat tcc agg cgc atc gaa aga atc	1219
Glu Glu Ala Ile Asn Ile Gln Gly Asp Ser Arg Arg Ile Glu Arg Ile	
360 365 370	
att cgc aac ctt cta gcc aat gcg atc gac cac tcc aag ggc ttg cct	1267
Ile Arg Asn Leu Leu Ala Asn Ala Ile Asp His Ser Lys Gly Leu Pro	
375 380 385	
gtt gag ttg aaa gtt gcc gac aac gtg gac gca gta gcg atc gtt gtt	1315
Val Glu Leu Lys Val Ala Asp Asn Val Asp Ala Val Ala Ile Val Val	
390 395 400 405	
att gat cac ggc gtc ggc ctg aaa cct gga caa gac gaa ttg gtg ttc	1363
Ile Asp His Gly Val Gly Leu Lys Pro Gly Gln Asp Glu Leu Val Phe	
410 415 420	
aac aga ttc tgg cga gcc gac cct tcg cgc gtc cgc cat tct ggt ggc	1411
Asn Arg Phe Trp Arg Ala Asp Pro Ser Arg Val Arg His Ser Gly Gly	
425 430 435	
acc ggc ctg ggt ctt gcg att tct cgc gaa gat gcg atg ctt cat gga	1459
Thr Gly Leu Gly Leu Ala Ile Ser Arg Glu Asp Ala Met Leu His Gly	
440 445 450	
gga aac ctt gat gcg gcg gga acg atc ggt gtt ggt tcc att ttc cgt	1507
Gly Asn Leu Asp Ala Ala Gly Thr Ile Gly Val Gly Ser Ile Phe Arg	
455 460 465	
ttg gtc ttg cct aaa gaa ccg cat gga aat tat cgt gaa gca ccg atc	1555
Leu Val Leu Pro Lys Glu Pro His Gly Asn Tyr Arg Glu Ala Pro Ile	
470 475 480 485	
ccg ttg atc gct cca gag aca ccg tgg gaa ggg gag cag cag	1597
Pro Leu Ile Ala Pro Glu Thr Pro Trp Glu Gly Glu Gln Gln	
490 495	
tgagtaaaat ttcgacgaaa ctg	1620

<210> 30

<211> 499

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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 Gly Leu Gly Met Leu Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys
 20 25 30
 Ile Asp Ile Ala Ser Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu
 35 40 45
 Glu Gln Ile Thr Ala Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val
 50 55 60
 Asn Ser Ala Arg Ala Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr
 65 70 75 80
 Glu Thr Asn Ala Ala Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp
 85 90 95
 Leu Val Val Ser Pro Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr
 100 105 110
 Phe Val Ser Glu Asn Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln
 115 120 125
 Gly Asp Gly Ser Ser Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu
 130 135 140
 Ser Asp Ile Pro Asn Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser
 145 150 155 160
 Asp Glu Ser Ser Leu Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu
 165 170 175
 Leu Ile Val Val Val Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln
 180 185 190
 Gln Val Thr Ala Pro Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe
 195 200 205
 Ala Gln Gly Lys Leu Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu
 210 215 220
 Met Ala Arg Leu Ala Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser
 225 230 235 240
 Ala Gln Ile Thr Lys Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe
 245 250 255
 Thr Ser Asp Val Ser His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg
 260 265 270
 Met Ala Ala Asp Leu Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly
 275 280 285
 Ala Arg Arg Ala Ser Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu
 290 295 300
 Ser Leu Leu Ser Asp Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val
 305 310 315 320
 Ala Glu Leu Ser Thr Ala Leu His Asp Val Arg Ile Pro Val Arg Ser

325								330				335			
Ala	Leu	Glu	Gln	Val	Gln	His	Leu	Ala	Thr	Glu	Leu	Asp	Val	Glu	Leu
			340						345				350		
Leu	Val	Asn	Leu	Pro	Glu	Glu	Ala	Ile	Asn	Ile	Gln	Gly	Asp	Ser	Arg
		355					360					365			
Arg	Ile	Glu	Arg	Ile	Ile	Arg	Asn	Leu	Leu	Ala	Asn	Ala	Ile	Asp	His
	370					375					380				
Ser	Lys	Gly	Leu	Pro	Val	Glu	Leu	Lys	Val	Ala	Asp	Asn	Val	Asp	Ala
385					390				395						400
Val	Ala	Ile	Val	Val	Ile	Asp	His	Gly	Val	Gly	Leu	Lys	Pro	Gly	Gln
			405						410					415	
Asp	Glu	Leu	Val	Phe	Asn	Arg	Phe	Trp	Arg	Ala	Asp	Pro	Ser	Arg	Val
		420							425				430		
Arg	His	Ser	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Arg	Glu	Asp
		435					440					445			
Ala	Met	Leu	His	Gly	Gly	Asn	Leu	Asp	Ala	Ala	Gly	Thr	Ile	Gly	Val
	450					455					460				
Gly	Ser	Ile	Phe	Arg	Leu	Val	Leu	Pro	Lys	Glu	Pro	His	Gly	Asn	Tyr
465					470					475					480
Arg	Glu	Ala	Pro	Ile	Pro	Leu	Ile	Ala	Pro	Glu	Thr	Pro	Trp	Glu	Gly
			485						490					495	

Glu Gln Gln

<210> 31
 <211> 1455
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1432)
 <223> RXN00651

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 catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115
 Met Gln Ser Ser Leu
 1 5
 gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163
 Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
 10 15 20
 gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211
 Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
 25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc	259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala	
40 45 50	
cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg	307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val	
55 60 65	
tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc	355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser	
70 75 80 85	
cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att	403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile	
90 95 100	
ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg	451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu	
105 110 115	
ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg	499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala	
120 125 130	
att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg	547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly	
135 140 145	
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc	595
Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr	
150 155 160 165	
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa	643
Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu	
170 175 180	
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg	691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala	
185 190 195	
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg	739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala	
200 205 210	
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg	787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met	
215 220 225	
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag	835
Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu	
230 235 240 245	
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca	883
Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr	
250 255 260	
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa	931
Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln	
265 270 275	
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc	979

Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 280 285 290

aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat 1027
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 295 300 305

gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct 1075
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 310 315 320 325

caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc 1123
 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 330 335 340

cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt 1171
 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 345 350 355

gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct 1219
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 360 365 370

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 375 380 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 390 395 400 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363
 Val Ser Ala Ala Leu Pro Val Glu Pro Glu Gly Phe Val Gly Ala
 410 415 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
 425 430 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att 1455
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<210> 32

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
 20 25 30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
 35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
 50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
 65 70 75 80
 Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
 85 90 95
 Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
 100 105 110
 Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
 115 120 125
 Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
 130 135 140
 Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
 145 150 155 160
 Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
 165 170 175
 Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
 180 185 190
 Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
 195 200 205
 Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
 210 215 220
 Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
 225 230 235 240
 Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
 245 250 255
 Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
 260 265 270
 Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
 275 280 285
 Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
 290 295 300
 Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr
 305 310 315 320
 Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser
 325 330 335
 Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val
 340 345 350
 Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val
 355 360 365
 Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln
 370 375 380

Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr
385 390 395 400

Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu
405 410 415

Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr
420 425 430

Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu
435 440

<210> 33

<211> 1455

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1432)

<223> FRXA00651

<400> 33

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catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115
Met Gln Ser Ser Leu
1 5

gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
10 15 20

gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc 259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
40 45 50

cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg 307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
55 60 65

tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc 355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
70 75 80 85

cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att 403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
90 95 100

ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg 451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
105 110 115

ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg 499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
120 125 130

att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly 135 140 145	547
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr 150 155 160 165	595
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu 170 175 180	643
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala 185 190 195	691
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala 200 205 210	739
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met 215 220 225	787
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu 230 235 240 245	835
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr 250 255 260	883
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln 265 270 275	931
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val 280 285 290	979
aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp 295 300 305	1027
gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala 310 315 320 325	1075
caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys 330 335 340	1123
cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val 345 350 355	1171
gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala 360 365 370	1219

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 375 380 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 390 395 400 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
 410 415 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
 425 430 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att 1455
 Ser Ser Pro Thr Asp Asp Glu
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<210> 34

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu
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Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
 20 25 30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
 35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
 50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
 65 70 75 80

Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
 85 90 95

Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
 100 105 110

Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
 115 120 125

Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
 130 135 140

Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
 145 150 155 160

Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
 165 170 175

Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr

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<210> 35
<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(535)
<223> RXA00006
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<400> 35

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agaagatggt cgcctatcca ccccgtagaa gaagataaaa atg gtc gat ttt gac 115
 Met Val Asp Phe Asp
 1 5

acc atc gca gcc cga ctt gtc acc gaa aca gaa gaa gca atc atc tac 163
 Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu Glu Ala Ile Ile Tyr
 10 15 20

gcc acc cgc gat gga ata atc aga ctc tgg aac ggc ggc tcc gag aaa 211
 Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn Gly Gly Ser Glu Lys
 25 30 35

ctc ttt gga tac acg gcc ggc gaa gcc ctt gga aaa tca ctc gac atc 259
 Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly Lys Ser Leu Asp Ile
 40 45 50

atc att ccc gaa aaa cac cgc aag gcc cac tgg gac gga tgg gat cgc 307
 Ile Ile Pro Glu Lys His Arg Lys Ala His Trp Asp Gly Trp Asp Arg
 55 60 65

gtc atg gaa tcc ggc gaa act cgc tat ggc tcc gaa ccg ctt aac gtt 355
 Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser Glu Pro Leu Asn Val
 70 75 80 85

cca ggc att cgt gcc gat gga tcc aaa atg tct ttg gaa ttc tcc atc 403
 Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser Leu Glu Phe Ser Ile
 90 95 100

acc atc ctg aag gac gat tcc gga aaa atc gaa ggc gtt gca gct ttt 451
 Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu Gly Val Ala Ala Phe
 105 110 115

ctc cgc gat gtc acc gcc aat tgg gat gag aaa aag gcc ctg cgg atc 499
 Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys Lys Ala Leu Arg Ile
 120 125 130

cga atc aaa gag ttg gaa cgc caa atc gag ggc cat taaggagatt 545
 Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly His
 135 140 145

cttgggtgcg cgg 558

<210> 36

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Val Asp Phe Asp Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu
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Glu Ala Ile Ile Tyr Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn
 20 25 30

Gly Gly Ser Glu Lys Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly
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Lys Ser Leu Asp Ile Ile Ile Pro Glu Lys His Arg Lys Ala His Trp
 50 55 60
 Asp Gly Trp Asp Arg Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser
 65 70 75 80
 Glu Pro Leu Asn Val Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser
 85 90 95
 Leu Glu Phe Ser Ile Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu
 100 105 110
 Gly Val Ala Ala Phe Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys
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 Lys Ala Leu Arg Ile Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly
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 His
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 Val Asn Pro Phe Ile
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 Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His Ala Gly Arg Asn Arg
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 gtt gcg gtg cgc aga gct gaa aac acc att gtc cgc tca gct aag ccc 211
 Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val Arg Ser Ala Lys Pro
 25 30 35
 gca ttc tca gtt gag gaa ctt tcg gag atc ctg gag tca cat tct att 259
 Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu Glu Ser His Ser Ile
 40 45 50
 cgc ctc gag ctg cag ccg atc cta gaa ctt gaa aca ggt cgg gtg ggt 307
 Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu Thr Gly Arg Val Gly
 55 60 65
 gca gcc gaa ggt ctg ctc cga atc aac ttg gat ggc acc gat gtt cct 355
 Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp Gly Thr Asp Val Pro
 70 75 80 85
 acg ggg cag ttt gtt cag tcg gtt gaa cag gcc ggg cta gcc ccg aag 403
 Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala Gly Leu Ala Pro Lys

90										95					100					
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Leu	Asp	Ile	Ala	Val	Met	Arg	Glu	Gly	Ile	Asn	His	Ile	Glu	Arg	Leu					
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aga	gct	gtg	tgt	ccg	act	ttc	agc	ctc	gct	ttg	aat	ctg	tcg	ggc	tat	499				
Arg	Ala	Val	Cys	Pro	Thr	Phe	Ser	Leu	Ala	Leu	Asn	Leu	Ser	Gly	Tyr					
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tct	ctg	agc	tcg	gcg	aaa	ata	cgg	gag	gaa	cta	aga	gcc	gaa	ttt	aga	547				
Ser	Leu	Ser	Ser	Ala	Lys	Ile	Arg	Glu	Glu	Leu	Arg	Ala	Glu	Phe	Arg					
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gct	cgc	gat	ctg	cca	agg	gga	tca	att	agg	ttt	gag	att	act	gag	acc	595				
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Lys	Asp	Phe	Gly	Phe	His	Ile	Val	Ile	Asp	Asp	Phe	Gly	Ala	Gly	His					
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gag	cct	tat	caa	tat	cta	aag	aag	ttc	gac	ttt	agc	gtg	ctg	aag	att	739				
Glu	Pro	Tyr	Gln	Tyr	Leu	Lys	Lys	Phe	Asp	Phe	Ser	Val	Leu	Lys	Ile					
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Ala	Gly	Glu	Phe	Ile	Glu	Gly	Met	Val	Thr	Asn	Arg	Val	Asp	Arg	Ser					
	215					220					225									
atc	gtc	gaa	tct	att	gct	caa	ctt	gct	aag	gat	gag	gag	atg	gaa	act	835				
Ile	Val	Glu	Ser	Ile	Ala	Gln	Leu	Ala	Lys	Asp	Glu	Glu	Met	Glu	Thr					
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gtc	gcc	gag	ttt	gtt	tca	agc	aag	gag	att	ttg	gag	gcg	gta	cga	gag	883				
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Ile	Asp	Glu	Phe	Ile	Ala	Thr	Tyr	Leu	Glu	Thr	Asn	Gln	Thr	Ala	Thr					
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Trp	Gly																			
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 Glu Ser His Ser Ile Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu
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 Thr Gly Arg Val Gly Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp
 65 70 75 80
 Gly Thr Asp Val Pro Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala
 85 90 95
 Gly Leu Ala Pro Lys Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn
 100 105 110
 His Ile Glu Arg Leu Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu
 115 120 125
 Asn Leu Ser Gly Tyr Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu
 130 135 140
 Arg Ala Glu Phe Arg Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe
 145 150 155 160
 Glu Ile Thr Glu Thr Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu
 165 170 175
 Phe Val Gln Met Leu Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp
 180 185 190
 Phe Gly Ala Gly His Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe
 195 200 205
 Ser Val Leu Lys Ile Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn
 210 215 220
 Arg Val Asp Arg Ser Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp
 225 230 235 240
 Glu Glu Met Glu Thr Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu
 245 250 255
 Glu Ala Val Arg Glu Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile
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Val Val Ala Arg Asp
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ctg cag aag ctg gaa aaa ctt cgc ctg att tgt gga tac gtg ttt cta 163
Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys Gly Tyr Val Phe Leu
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gtc cca gcc ata tac ctg cac ttt ttt gcg gaa acc tcc ctc agg gga 211
Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu Thr Ser Leu Arg Gly
25 30 35

gtg att ctg gca gga att gcg cac gct atc gca ggt cct ggc gtt gca 259
Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala Gly Pro Gly Val Ala
40 45 50

ctg gtt atg gca ttc atg gaa aat gcg caa ttg cca gaa ctg ttg cgt 307
Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu Pro Glu Leu Leu Arg
55 60 65

aaa cgg cat gca ttc gca ccc ttc tcc cat att cgc ctt cca ggc gat 355
Lys Arg His Ala Phe Ala Pro Phe Ser His Ile Arg Leu Pro Gly Asp
70 75 80 85

gta ttc cgg ctc ctc gtc gcg ggc att gtc atg gtc gca ata tcc aaa 403
Val Phe Arg Leu Leu Val Ala Gly Ile Val Met Val Ala Ile Ser Lys
90 95 100

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Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu Thr Gly Ile Ile Val
120 125 130

gtt gcc ggg ccc gga att gca ctt tcg acg ccg ctg gta cta aat att 547
Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro Leu Val Leu Asn Ile
135 140 145

cac cga tca gca tgg cgc gag ttc gca gtt gtt atc ata gct acg gtc 595
 His Arg Ser Ala Trp Arg Glu Phe Ala Val Val Ile Ile Ala Thr Val
 150 155 160 165

gga gtg ctg gcg ctc att ttc gga ttt gct gtg gat ctt ccg acg gtc 643
Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val Asp Leu Pro Thr Val
170 175 180

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Tyr	Leu	Ala	Met	Leu	Pro	Leu	Tyr	Trp	Ser	Ala	Thr	Arg	Leu	Pro	Val	
			185					190					195			

ctt tta gcc gtt ctt cat gcg gtg ttt act tca gca ata gtc gta att	739
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ctg tat ttc cta tta ggt acc gga tct ttt gcg att acg gat gaa tcc	787
Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala Ile Thr Asp Glu Ser	
215 220 225	
ata ctg gtg cag gca acg aca att cag ctt ttt gtt ctg atg tgt atc	835
Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe Val Leu Met Cys Ile	
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Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln Gln Thr Ser Ala Leu	
250 255 260	
gtt gaa gag cta gag gtg gta gcg aag acc ctt cct gat gcg ctt ttt	931
Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu Pro Asp Ala Leu Phe	
265 270 275	
atc gta aac aaa aat gga aca gca ttt cct gtt aac gca ggc gcg aaa	979
Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val Asn Ala Gly Ala Lys	
280 285 290	
aat ttc gtc aag caa tca ccg gat ggg cat tat tcc atg ccg aaa cta	1027
Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr Ser Met Pro Lys Leu	
295 300 305	
cag aat ata gac ggt gaa ccc atg gat gag aaa gaa agt ccg agc agt	1075
Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys Glu Ser Pro Ser Ser	
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atg gcc ttg cgt gga caa ggt gtc gaa gga gta tta gcc aag tta ggt	1123
Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val Leu Ala Lys Leu Gly	
330 335 340	
gaa gta ctg gga gaa gat ccg gac ttg gcg cgt cga atc ttc gaa att	1171
Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg Arg Ile Phe Glu Ile	
345 350 355	
agt gcc tca ccg atg tat ctg cgt gga gaa act gaa ccg ggt cat gcg	1219
Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr Glu Pro Gly His Ala	
360 365 370	
ctc gtg att tgg cat gac agt act aat gag tat tac acg atg caa caa	1267
Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr Tyr Thr Met Gln Gln	
375 380 385	
ttg acg ctt gca tat gaa gaa tcg cgg ctg cta ttt gaa aaa gcc cct	1315
Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu Phe Glu Lys Ala Pro	
390 395 400 405	
caa ggg att gcc atg ctg gac cct tcg gga gaa atc gta atg gcg aat	1363
Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu Ile Val Met Ala Asn	
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cga tcc ttt ggt gac ttg gtg gga acg act cct gtt cga ctc cta gga	1411
Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro Val Arg Leu Leu Gly	
425 430 435	

cga aat cta gag gat ttc gga gta gag gag gga acc atg gaa tac gtg	1459
Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly Thr Met Glu Tyr Val	
440 445 450	
acc cct gtt ctg tcg gac cca gaa gcc gtt gtg cac tta gat cgt tcg	1507
Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val His Leu Asp Arg Ser	
455 460 465	
ctc gaa aca ttg aga ggt aaa cag aaa aac gtt gct atg tca ttt agc	1555
Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val Ala Met Ser Phe Ser	
470 475 480 485	
tcg atg ggc aat gtt gga ggc aga atc gga act tta ctc gtt aat gtt	1603
Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr Leu Leu Val Asn Val	
490 495 500	
gtc gat gta acc gag cgc caa gaa ctc atc gag ctt gtg gag cat ttg	1651
Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu Leu Val Glu His Leu	
505 510 515	
gcg gat cat gac tcc ctg aca gga ttg gtc aat cgc agg cgg ctg gaa	1699
Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn Arg Arg Arg Leu Glu	
520 525 530	
tct gat atc gaa gag ctt atc ctc aag aat gaa cgc gat tcg acc gat	1747
Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu Arg Asp Ser Thr Asp	
535 540 545	
agt gca ttg ttg ctt ttg gat ctg gat tac ttc aag gaa gtt aat gat	1795
Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe Lys Glu Val Asn Asp	
550 555 560 565	
tcc ctc ggc cat gag gct ggt gac cag ttg ctt att gag ttt gct gag	1843
Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu Ile Glu Phe Ala Glu	
570 575 580	
atc ctc aaa gac agc gtg agg gat tcc gac att gtc gga cgc atc ggc	1891
Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile Val Gly Arg Ile Gly	
585 590 595	
ggc gat gaa ttc gtt att gtt ttg cct gac aca gac agg gat ggc gct	1939
Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr Asp Arg Asp Gly Ala	
600 605 610	
gaa gca atc ggt ata aga att att gag ttg gtc aat cag cac ttc aaa	1987
Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val Asn Gln His Phe Lys	
615 620 625	
ggc cga gga aaa gtg tta tcg cgg gtg tca agt aaa gta tcg gcg gga	2035
Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser Lys Val Ser Ala Gly	
630 635 640 645	
cgc tct ttt ctg atg ctc gtg ccc aag gtg tgaatccatt cattcttgct	2085
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gat	2088

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<213> *Corynebacterium glutamicum*

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Thr Ser Leu Arg Gly Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala
 35 40 45

Gly Pro Gly Val Ala Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu
 50 55 60

Pro Glu Leu Leu Arg Lys Arg His Ala Phe Ala Pro Phe Ser His Ile
 65 70 75 80

Arg Leu Pro Gly Asp Val Phe Arg Leu Leu Val Ala Gly Ile Val Met
 85 90 95

Val Ala Ile Ser Lys Leu Ile Val Ile Leu Ala Tyr Ala Leu Ala Asp
 100 105 110

Leu Pro Tyr Ser Phe Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu
 115 120 125

Thr Gly Ile Ile Val Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro
 130 135 140

Leu Val Leu Asn Ile His Arg Ser Ala Trp Arg Glu Phe Ala Val Val
 145 150 155 160

Ile Ile Ala Thr Val Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val
 165 170 175

Asp Leu Pro Thr Val Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala
 180 185 190

Thr Arg Leu Pro Val Leu Leu Ala Val Leu His Ala Val Phe Thr Ser
 195 200 205

Ala Ile Val Val Ile Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala
 210 215 220

Ile Thr Asp Glu Ser Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe
 225 230 235 240

Val Leu Met Cys Ile Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln
 245 250 255

Gln Thr Ser Ala Leu Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu
 260 265 270

Pro Asp Ala Leu Phe Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val
 275 280 285

Asn Ala Gly Ala Lys Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr
 290 295 300

Ser Met Pro Lys Leu Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys
 305 310 315 320
 Glu Ser Pro Ser Ser Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val
 325 330 335
 Leu Ala Lys Leu Gly Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg
 340 345 350
 Arg Ile Phe Glu Ile Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr
 355 360 365
 Glu Pro Gly His Ala Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr
 370 375 380
 Tyr Thr Met Gln Gln Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu
 385 390 395 400
 Phe Glu Lys Ala Pro Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu
 405 410 415
 Ile Val Met Ala Asn Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro
 420 425 430
 Val Arg Leu Leu Gly Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly
 435 440 445
 Thr Met Glu Tyr Val Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val
 450 455 460
 His Leu Asp Arg Ser Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val
 465 470 475 480
 Ala Met Ser Phe Ser Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr
 485 490 495
 Leu Leu Val Asn Val Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu
 500 505 510
 Leu Val Glu His Leu Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn
 515 520 525
 Arg Arg Arg Leu Glu Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu
 530 535 540
 Arg Asp Ser Thr Asp Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe
 545 550 555 560
 Lys Glu Val Asn Asp Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu
 565 570 575
 Ile Glu Phe Ala Glu Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile
 580 585 590
 Val Gly Arg Ile Gly Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr
 595 600 605
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Met Thr Ala Leu Ile															5
1															
cca gct cgc cac agc ctg act ttt cgt ctg ctc acc gcg cag ctt gct															163
Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu Thr Ala Gln Leu Ala															20
10 15															
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Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile Val Ala Ala Leu Val															35
25 30															
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Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu Ser Gly Pro Ile Asp															50
40 45															
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Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala Tyr Arg Asp Ala Asn															65
55 60															
tac att gcc ctc gca gcg gca ctt ccc acc gca gtg ttg agc tcc att															355
Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala Val Leu Ser Ser Ile															85
70 75															
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Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly Gln Pro Leu Trp Arg															95
90 95															
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Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly Asp Tyr Gln Val Arg															115
105 110															
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Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala Ala Leu Ser Leu Ala															120
125 130															
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Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr Glu Glu Leu Arg Arg															145
135 140 145															
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Asn Met Leu Ser Asp Leu Ser His Glu Met Asn Thr Pro Leu Ser Val															

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Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly Met Val Glu Trp Asp				
170	175	180		
gcc gac acc cac gca gtt ttc gcc gag caa ctt ggc cgg ctt tcc cgc	691			
Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu Gly Arg Leu Ser Arg				
185	190	195		
ctc aca tca gat ctt gat gat gtc tct aga gcc caa gaa cac cgc ttc	739			
Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala Gln Glu His Arg Phe				
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gac ctg gtc tac agc acc gtc gcc atc ggt ggt ctc att cac aat gcc	787			
Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly Leu Ile His Asn Ala				
215	220	225		
gcc gga gcc gcc gca ggt tcc tac caa gaa aaa ggc gtg gcc ctg gaa	835			
Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys Gly Val Ala Leu Glu				
230	235	240	245	
gta aca ggc agc gat tcc acc gaa ctc atc cgc gtt gat agc caa cgc	883			
Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg Val Asp Ser Gln Arg				
250	255	260		
ttc gcc caa gtc atg gcc aac ctc ttc tcc aac gcc ttg cgg cac acc	931			
Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn Ala Leu Arg His Thr				
265	270	275		
ccc gcc ggt ggg aaa gtt cac gtc cgc gtc ctg cgt caa ggc gtg gga	979			
Pro Ala Gly Gly Lys Val His Val Arg Val Leu Arg Gln Gly Val Gly				
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Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu Gly Ile Ala Pro Glu				
295	300	305		
cac gta aaa tac gtt ttc gaa cgc tac ttc cgc gcc aaa cga tcc gac	1075			
His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg Ala Lys Arg Ser Asp				
310	315	320	325	
tcc gac gac caa tcc ggc tcc gga atc ggc ctc acc atc tcc cgc gca	1123			
Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu Thr Ile Ser Arg Ala				
330	335	340		
ctc atc gaa gcg caa ggt ggc aca cta acc gca gaa tcc gct ggc ctg	1171			
Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala Glu Ser Ala Gly Leu				
345	350	355		
ggc aaa ggc gcg aaa ttt acc atc cga cta ccc ctt tta agc aaa	1216			
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<210> 42

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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			20					25					30		
Val	Ala	Ala	Leu	Val	Gly	Pro	Ala	Ile	Phe	Asn	Ser	His	Leu	Asp	Leu
		35					40					45			
Ser	Gly	Pro	Ile	Asp	Pro	Arg	Gln	Thr	Asp	Phe	His	Ile	Gln	Glu	Ala
	50					55					60				
Tyr	Arg	Asp	Ala	Asn	Tyr	Ile	Ala	Leu	Ala	Ala	Ala	Leu	Pro	Thr	Ala
	65				70					75					80
Val	Leu	Ser	Ser	Ile	Gly	Val	Ser	Phe	Trp	Leu	Ser	His	Arg	Leu	Gly
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Gln	Pro	Leu	Trp	Arg	Leu	Ser	Arg	Ala	Ala	Thr	Ala	Met	Ser	Ser	Gly
			100					105					110		
Asp	Tyr	Gln	Val	Arg	Val	Pro	Ile	Ser	Asp	Val	Asp	Lys	Glu	Val	Ala
		115					120					125			
Ala	Leu	Ser	Leu	Ala	Phe	Asn	Ser	Met	Ala	Asp	Gln	Leu	Glu	His	Thr
	130					135					140				
Glu	Glu	Leu	Arg	Arg	Asn	Met	Leu	Ser	Asp	Leu	Ser	His	Glu	Met	Asn
145					150					155					160
Thr	Pro	Leu	Ser	Val	Leu	Leu	Val	Tyr	Val	Asp	Gly	Leu	Gln	Asp	Gly
				165					170						175
Met	Val	Glu	Trp	Asp	Ala	Asp	Thr	His	Ala	Val	Phe	Ala	Glu	Gln	Leu
			180					185					190		
Gly	Arg	Leu	Ser	Arg	Leu	Thr	Ser	Asp	Leu	Asp	Asp	Val	Ser	Arg	Ala
		195					200					205			
Gln	Glu	His	Arg	Phe	Asp	Leu	Val	Tyr	Ser	Thr	Val	Ala	Ile	Gly	Gly
	210					215					220				
Leu	Ile	His	Asn	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Ser	Tyr	Gln	Glu	Lys
225				230						235					240
Gly	Val	Ala	Leu	Glu	Val	Thr	Gly	Ser	Asp	Ser	Thr	Glu	Leu	Ile	Arg
				245					250					255	
Val	Asp	Ser	Gln	Arg	Phe	Ala	Gln	Val	Met	Ala	Asn	Leu	Phe	Ser	Asn
			260					265					270		
Ala	Leu	Arg	His	Thr	Pro	Ala	Gly	Gly	Lys	Val	His	Val	Arg	Val	Leu
		275					280					285			
Arg	Gln	Gly	Val	Gly	Thr	Ile	Val	Ile	Glu	Val	Ile	Asp	Asn	Gly	Glu
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ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115															
Met Asn Lys Asp Phe 5															
tgg acc gca ggc tgg acc gcc cgc tgg ttt tgc cgc ggg gtt tcc ctt 163															
Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu 20															
ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct 211															
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro 35															
aac ttg gcc aag tac acc ctc tac acc agg gtg tgc ttg caa gcg atc 259															
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile 50															
ccc gtg gtg ttg ctg tgc gcg tat ttc ctg ggc atc gta gct aat gca 307															
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala 65															
ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tgc gtc atc 355															
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile 85															
ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tgc ctg aat 403															
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn 100															
tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg 451															
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val 115															
ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc 499															
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly															

120	125	130	
tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu 135 140 145			547
acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr 150 155 160 165			595
cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser 170 175 180			643
aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu 185 190 195			691
atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys 200 205 210			739
gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu 215 220 225			787
gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His 230 235 240 245			835
ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys 250 255 260			883
cgc ggc gac gac cgc ctc gaa aac gag ctg cgt gag ctc caa aaa ctc Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg Glu Leu Gln Lys Leu 265 270 275			931
acc cgc acc tcc atg tcg gaa atg cgc gac gtc gtc tcc ggc tac cgc Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val Val Ser Gly Tyr Arg 280 285 290			979
acc gtc aac ctc gcc acg gaa atc gag ggc gct aaa agt ttg ctt gcc Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala Lys Ser Leu Leu Ala 295 300 305			1027
gac gcc cac atc cac ctt tcc gtc atc ggc acc acg tcc cag gtg tca Asp Ala His Ile His Leu Ser Val Ile Gly Thr Thr Ser Gln Val Ser 310 315 320 325			1075
ccc gct cac cga gaa ctg tgc gcg tgg ctt gtc cgg gaa gcc acc aca Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val Arg Glu Ala Thr Thr 330 335 340			1123
aac att ctg cgc cac tct gat gca acg gat gcc acc ctc acg ttg agc Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala Thr Leu Thr Leu Ser 345 350 355			1171
agc aca gag gtg cgc atg gac aac aat ggt gtg aac aag gac atc ggc Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val Asn Lys Asp Ile Gly 360 365 370			1219

aga ctc tct ggt ctc agc gcc ctg cgc tca cga gcg gaa tca gcc gga 1267
 Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg Ala Glu Ser Ala Gly
 375 380 385

atg acg ctc att gtg tcc cgc gaa gac gac cag ttc agc gtc cgc atg 1315
 Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln Phe Ser Val Arg Met
 390 395 400 405

ctc att aat gca cct gca aat aca cct gca gaa aag gaa gct 1357
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 410 415

taaatgattt ccatttccat cgc 1380

<210> 44

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

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Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser
 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
 180 185 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
 195 200 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
 210 215 220
 Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
 225 230 235 240
 Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
 245 250 255
 Leu Ala Leu Ala Lys Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg
 260 265 270
 Glu Leu Gln Lys Leu Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val
 275 280 285
 Val Ser Gly Tyr Arg Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala
 290 295 300
 Lys Ser Leu Leu Ala Asp Ala His Ile His Leu Ser Val Ile Gly Thr
 305 310 315 320
 Thr Ser Gln Val Ser Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val
 325 330 335
 Arg Glu Ala Thr Thr Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala
 340 345 350
 Thr Leu Thr Leu Ser Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val
 355 360 365
 Asn Lys Asp Ile Gly Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg
 370 375 380
 Ala Glu Ser Ala Gly Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln
 385 390 395 400
 Phe Ser Val Arg Met Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu
 405 410 415
 Lys Glu Ala

<210> 45
 <211> 895
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(895)
 <223> FRXA01211

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 ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115
 Met Asn Lys Asp Phe
 1 5
 tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt 163

Trp	Thr	Ala	Gly	Trp	Thr	Ala	Arg	Trp	Phe	Ser	Arg	Gly	Val	Ser	Leu	
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Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro																
	25			30					35							
aac ttg gcc aag tac acc ctc tac acc agg gtg tcg ttg caa gcg atc	259															
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile																
	40			45					50							
ccc gtg gtg ttg ctg tcg gcg tat ttc ctg ggc atc gta gct aat gca	307															
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala																
	55			60					65							
ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tcg gtc atc	355															
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile																
	70			75					80						85	
ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tcg ctg aat	403															
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn																
	90			95					100							
tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg	451															
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val																
	105			110					115							
ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc	499															
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly																
	120			125					130							
tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt	547															
Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu																
	135			140					145							
acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac	595															
Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr																
	150			155					160						165	
cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc	643															
Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser																
	170			175					180							
aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc	691															
Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu																
	185			190					195							
atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa	739															
Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys																
	200			205					210							
gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa	787															
Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu																
	215			220					225							
gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac	835															
Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His																
	230			235					240						245	
ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa	883															
Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys																

250

255

260

cgc ggc gac gac
 Arg Gly Asp Asp
 265

895

<210> 46
 <211> 265
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 46

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Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser
 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
 180 185 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
 195 200 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
 210 215 220

Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
 225 230 235 240

Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
 245 250 255

Leu Ala Leu Ala Lys Arg Gly Asp Asp
 260 265

<210> 47
 <211> 529
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(529)
 <223> RXA01248

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 Met Ala Asp Arg Thr
 1 5
 ccg acc acc gcc acg ccc ccg ggg cgg gtg ctg gtc gtc gat gat gaa 163
 Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu Val Val Asp Asp Glu
 10 15 20
 caa ccc ctg gct cag atg gtg gcc tcc tac ctc atc cgg gcc ggc attc 211
 Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu Ile Arg Ala Gly Phe
 25 30 35
 gac acc cgc cag gcg cac acc ggc acc cag gcc gtg gac gag gcc cgt 259
 Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala Val Asp Glu Ala Arg
 40 45 50
 cgc ttt tcc ccc gat gtt gtg gtg ctg gat ctg ggg ctg ccc gaa ctc 307
 Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu Gly Leu Pro Glu Leu
 55 60 65
 gac ggc ctg gag gtg tgc cga cgg atc cgc acc ttc tcg gac tgc tac 355
 Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr Phe Ser Asp Cys Tyr
 70 75 80 85
 atc ctc atg ctc acc gcg cgt ggc agc gag gac gac aag atc agc ggt 403
 Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp Asp Lys Ile Ser Gly
 90 95 100
 ttg acc ctg ggg gcg gat gac tac atc acc aaa cct ttt agc atc cgg 451
 Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Ser Ile Arg
 105 110 115
 gaa ctg gtg acc cgg gtg cat gcg gtg ctg cgc cgc ccg cgc acc agc 499
 Glu Leu Val Thr Arg Val His Ala Val Leu Arg Arg Pro Arg Thr Ser
 120 125 130
 acc acc cca ccg cag gtg acc acc ccc ttg 529
 Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
 135 140

<210> 48
 <211> 143
 <212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Val Val Asp Asp Glu Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu
 20 25 30

Ile Arg Ala Gly Phe Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala
 35 40 45

Val Asp Glu Ala Arg Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu
 50 55 60

Gly Leu Pro Glu Leu Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr
 65 70 75 80

Phe Ser Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp
 85 90 95

Asp Lys Ile Ser Gly Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys
 100 105 110

Pro Phe Ser Ile Arg Glu Leu Val Thr Arg Val His Ala Val Leu Arg
 115 120 125

Arg Pro Arg Thr Ser Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
 130 135 140

<210> 49

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA02668

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 Met Thr Asn Pro Ser
 1 5

ccc gcg cta aat gaa acc ctt tcc ggc agg gtg ctg atc gtt gaa gat 163
 Pro Ala Leu Asn Glu Thr Leu Ser Gly Arg Val Leu Ile Val Glu Asp
 10 15 20

gag cgc cct ctt gct cgc atg att tgc ctt tat tta agc aaa gcg ggt 211
 Glu Arg Pro Leu Ala Arg Met Ile Ser Leu Tyr Leu Ser Lys Ala Gly
 25 30 35

ttc gat acc acc acg atc cac gac ggc gcc gct gct cca gat aag gtc 259
 Phe Asp Thr Thr Thr Ile His Asp Gly Ala Ala Ala Pro Asp Lys Val
 40 45 50

gct cac ctg cgc ccc gac gtg gtc att ttg gat ctt ggg ctg cct ggt 307

Ala	His	Leu	Arg	Pro	Asp	Val	Val	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Gly		
55						60					65						
ctt	gat	ggt	ttg	gaa	gtg	tgc	aaa	cgc	atc	cgc	gcg	ttc	acc	gat	tgc	355	
Leu	Asp	Gly	Leu	Glu	Val	Cys	Lys	Arg	Ile	Arg	Ala	Phe	Thr	Asp	Cys		
70					75				80						85		
tac	atc	cta	atg	ctc	acc	gcc	agg	ggt	tca	gag	cgg	gat	cgg	att	aca	403	
Tyr	Ile	Leu	Met	Leu	Thr	Ala	Arg	Gly	Ser	Glu	Arg	Asp	Arg	Ile	Thr		
				90					95					100			
ggt	ttg	gaa	att	ggg	gct	gat	gat	tac	atc	acc	aag	ccg	ttt	aat	atc	451	
Gly	Leu	Glu	Ile	Gly	Ala	Asp	Asp	Tyr	Ile	Thr	Lys	Pro	Phe	Asn	Ile		
			105					110					115				
cgc	gaa	ctt	gtc	att	cgt	atc	cag	tca	gta	atg	cgt	cgc	cct	cga	aaa	499	
Arg	Glu	Leu	Val	Ile	Arg	Ile	Gln	Ser	Val	Met	Arg	Arg	Pro	Arg	Lys		
		120					125					130					
atc	gat	gaa	acc	atc	caa	aat	ggt	ttg	acc	ttg	act	tat	ggc	cac	att	547	
Ile	Asp	Glu	Thr	Ile	Gln	Asn	Gly	Leu	Thr	Leu	Thr	Tyr	Gly	His	Ile		
		135				140					145						
gag	ctg	gac	acc	ttg	gcg	cat	gaa	gtc	act	gtc	aaa	ggc	gtt	ggg	gtg	595	
Glu	Leu	Asp	Thr	Leu	Ala	His	Glu	Val	Thr	Val	Lys	Gly	Val	Gly	Val		
150					155					160					165		
aca	ctg	acc	cgc	aca	gaa	ttt	gag	ctg	ctt	caa	gcc	ctc	atg	cac	aaa	643	
Thr	Leu	Thr	Arg	Thr	Glu	Phe	Glu	Leu	Leu	Gln	Ala	Leu	Met	His	Lys		
				170					175					180			
ccg	gga	gag	gca	gtg	tct	agg	cgt	gat	ttg	gtc	agc	caa	gtg	tgg	gat	691	
Pro	Gly	Glu	Ala	Val	Ser	Arg	Arg	Asp	Leu	Val	Ser	Gln	Val	Trp	Asp		
			185					190						195			
acc	acc	tgg	gtt	ggc	gat	gaa	cgc	atc	gtt	gac	gtg	cac	att	gga	aat	739	
Thr	Thr	Trp	Val	Gly	Asp	Glu	Arg	Ile	Val	Asp	Val	His	Ile	Gly	Asn		
		200					205					210					
ctg	cgc	cgc	aag	ctg	gaa	gca	cct	gcg	ccg	ggt	tca	cac	ttc	atc	gac	787	
Leu	Arg	Arg	Lys	Leu	Glu	Ala	Pro	Ala	Pro	Gly	Ser	His	Phe	Ile	Asp		
		215				220					225						
acc	atc	cga	ggt	gtt	ggc	tac	cgg	atg	gcc	ttc	aaa	tgacagccct				833	
Thr	Ile	Arg	Gly	Val	Gly	Tyr	Arg	Met	Ala	Phe	Lys						
230					235					240							
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<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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Leu	Ile	Val	Glu	Asp	Glu	Arg	Pro	Leu	Ala	Arg	Met	Ile	Ser	Leu	Tyr		
		20						25					30				

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<400> 51
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gaggaagtct gtcacggact ggaagacgaa aagggtatcg atg aaa att tta gtt 115
Met Lys Ile Leu Val
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Phe Asn Gly Tyr Asn Val Val Leu Ala Glu Asp Gly Ile Gln Ala Leu	
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Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val Ile Leu Asp Val Met	
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Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp Asp Tyr Leu Ala Lys	
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Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val Arg Ser Leu Val Arg	
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Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser Ile Glu Gln Ala Leu	
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Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu Ser Arg Asp Val Tyr	
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Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr Glu Phe Ala Leu Leu	
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Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu Thr Arg Ala Gln Ile	
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Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr Ser Gly Asn Ala Leu	
185 190 195	
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Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr Glu Leu Glu Gly Glu	
200 205 210	
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Asp Arg Leu Ile His Thr Val Arg Gly Val Gly Tyr Val Leu Arg Glu	
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 Ile Leu Asp Val Met Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg
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 His Leu Arg Ser Glu Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala
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 Asp Tyr Leu Ala Lys Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val
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 Arg Ser Leu Val Arg Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser
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 Ser Arg Asp Val Tyr Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr
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 Glu Phe Ala Leu Leu Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu
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 Thr Arg Ala Gln Ile Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr
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 Ser Gly Asn Ala Leu Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr
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 <223> RXA02631

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Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala Phe Ala Val Gly Val
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Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser Tyr Val Thr Asn Ser
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Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr Glu Ile Ala Leu Leu
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Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu Ile Pro Pro Gly Trp
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Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val Thr Ser Ala Glu Arg
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Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val Val Val Phe Ala Lys
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Glu Ile Ala Leu Leu Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu
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Ile Pro Pro Gly Trp Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro
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Asp Ser Asp Phe Leu Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val
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Thr Ser Ala Glu Arg Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val
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Val Val Phe Ala Lys Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val
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Leu Gly Val Ile Leu Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser
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Ile Leu Leu Gly Phe Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser
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Lys Leu Gln Arg Ala Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg
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Ala Ile Pro Val Val Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser
 195 200 205

Phe Asn Asp Met Leu Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser
 210 215 220

Gln Leu Val Ala Asp Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser
 225 230 235 240

Met Arg Thr Asn Ile Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly
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Ser Gly Ile Pro Lys Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu
 260 265 270

Ala Gln Met Thr Glu Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu

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Lys	Ala	Thr	Val	Arg	Ile	Val	Ile	Asp	Asp	Ser	Gly	Pro	Gly	Ile	Ala
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Ser	Arg	Ser	Met	Pro	Gly	Ser	Gly	Leu	Gly	Leu	Ala	Ile	Val	Asn	Gln
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 Met Ser Lys Ile Leu
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 Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu Ser Gly Ala Glu Ala
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ttc gcc cgc gca cat tcc ggc gat ttc gat ctc atg gtt tta gac ctc 259
 Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu Met Val Leu Asp Leu
 40 45 50

ggc ctc ccc cac atg gac ggc acg gat gtc cta gag caa tta aga aat 307
 Gly Leu Pro His Met Asp Gly Thr Asp Val Leu Glu Gln Leu Arg Asn
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gag gac cgc ctc cgc acc ctc gag ggc ggc gcc gac gat tac atg ccc 403
 Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala Asp Asp Tyr Met Pro
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 Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg Ile Lys Leu Arg Leu
 105 110 115

gcc aaa cac act cct cag gaa acg ccg acc gat gcg cgc gtg cta cga 499
 Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp Ala Arg Val Leu Arg
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aac ggc gat ttg gag ctc gat ctt cgt acc cag cgt gtg ctc atc gac 547
 Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln Arg Val Leu Ile Asp
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ggc tcc tgg cac gac ctt tcc cgc cgc gaa gtc gat ctg ctc gaa acc 595
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 170 175 180

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tat atc cgc gcg ttg agg aag aaa atc ggt gcc cat cgg gtc gaa acc 739
 Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala His Arg Val Glu Thr
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<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Met Val Leu Asp Leu Gly Leu Pro His Met Asp Gly Thr Asp Val Leu
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Glu Gln Leu Arg Asn Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr
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Ala Arg Thr Asn Ile Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala
85 90 95

Asp Asp Tyr Met Pro Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg
100 105 110

Ile Lys Leu Arg Leu Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp
115 120 125

Ala Arg Val Leu Arg Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln
130 135 140

Arg Val Leu Ile Asp Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val
145 150 155 160

Asp Leu Leu Glu Thr Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg
165 170 175

Val Gln Leu Leu Arg Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser
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<223> RXA00284

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Met Ala Arg Lys Leu
1 5

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Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile Val Glu Ser Gly Asp
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Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg Ala Leu Asp Ala Lys

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Ser	Pro	Asp	Phe	Leu	Leu	Lys	Arg	Gly	Ala	Asp	Val	Cys	Ala	Val	Asn					
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Tyr	Asp	Leu	Leu	Val	Pro	Ala	Met	Gly	Lys	Ala	Lys	Ser	Leu	Gln	Gly					
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 Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg Met Ala Lys Ser Leu
 280 285 290
 aac cac att tgt gag cag ggc gtt cct ttg ggt gag cca gaa tta gaa 1027
 Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly Glu Pro Glu Leu Glu
 295 300 305
 gaa ctg gct gcg gcc gtt aaa tca gtg cgc aaa gga gaa ccc acc gag 1075
 Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys Gly Glu Pro Thr Glu
 310 315 320 325
 gag gag atc gac acc ctt cca cgg ttg gcc acc aaa tgg gtc gca caa 1123
 Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr Lys Trp Val Ala Gln
 330 335 340
 aac cca caa ccg ctg cca ctg gga gag gtt gac tac aag cgc 1165
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 <213> Corynebacterium glutamicum

<400> 58
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 Val Glu Ser Gly Asp Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg
 20 25 30
 Ala Leu Asp Ala Lys Asn Arg His Gly Asn Thr Ala Leu His Met Arg
 35 40 45
 Gly Val Pro Glu Glu Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp
 50 55 60
 Val Asp Ile Arg Asn Glu Asp Gly Asp Thr Pro Leu His Val His Ser
 65 70 75 80
 His Asp Trp Asn Leu Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp
 85 90 95
 Val Cys Ala Val Asn Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala
 100 105 110
 Phe Phe Pro Glu Asn Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro
 115 120 125
 Tyr Ser Arg Ala Asn Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg
 130 135 140
 Ser Ala Asp Thr Gly Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu
 145 150 155 160
 Leu Ser Gly Thr Glu Phe Thr Asp Ala Glu Phe Arg Glu Thr Gln Glu

ctg cag tgg atc atc gga cac ggt ggc atg tcc acc gta tgg ctc gca 211

Leu	Gln	Trp	Ile	Ile	Gly	His	Gly	Gly	Met	Ser	Thr	Val	Trp	Leu	Ala		
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gat	gat	gtg	gtc	aat	gat	cgc	gaa	gta	gcc	atc	aag	gta	ctg	cgc	ccg	259	
Asp	Asp	Val	Val	Asn	Asp	Arg	Glu	Val	Ala	Ile	Lys	Val	Leu	Arg	Pro		
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gaa	ttt	tcc	gac	aac	cag	gag	ttc	ttg	aac	cgt	ttc	cgc	aat	gaa	gcg	307	
Glu	Phe	Ser	Asp	Asn	Gln	Glu	Phe	Leu	Asn	Arg	Phe	Arg	Asn	Glu	Ala		
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Gln	Ala	Ala	Glu	Asn	Ile	Asp	Ser	Glu	His	Val	Val	Ala	Thr	Tyr	Asp		
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tac	cgt	gag	gtt	cca	gac	cct	gct	ggg	cat	act	ttc	tgc	ttc	atc	gtc	403	
Tyr	Arg	Glu	Val	Pro	Asp	Pro	Ala	Gly	His	Thr	Phe	Cys	Phe	Ile	Val		
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atg	gaa	ttt	gtc	cgc	ggg	gaa	tcg	ctt	gcg	gat	ctt	cta	gag	cgc	gaa	451	
Met	Glu	Phe	Val	Arg	Gly	Glu	Ser	Leu	Ala	Asp	Leu	Leu	Glu	Arg	Glu		
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Gly	Arg	Leu	Pro	Glu	Asp	Leu	Ala	Leu	Asp	Val	Met	Glu	Gln	Ala	Ala		
		120					125					130					
cat	ggg	ttg	tcg	gtg	att	cac	cgg	atg	gac	atg	gtg	cac	cgc	gat	atc	547	
His	Gly	Leu	Ser	Val	Ile	His	Arg	Met	Asp	Met	Val	His	Arg	Asp	Ile		
	135					140					145						
aag	ccg	ggc	aac	atg	ctg	atc	aca	gcc	aat	ggc	att	gtg	aag	atc	acg	595	
Lys	Pro	Gly	Asn	Met	Leu	Ile	Thr	Ala	Asn	Gly	Ile	Val	Lys	Ile	Thr		
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Asp	Phe	Gly	Ile	Ala	Lys	Ala	Ala	Ala	Ala	Val	Pro	Leu	Thr	Arg	Thr		
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ggc	atg	gtg	gtg	ggg	act	gct	caa	tat	gtt	tca	cct	gag	caa	gcc	cag	691	
Gly	Met	Val	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Gln	Ala	Gln		
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ggc	aag	gaa	gtc	acc	gcg	gct	tct	gat	att	tat	tct	ctc	ggg	gtg	gtc	739	
Gly	Lys	Glu	Val	Thr	Ala	Ala	Ser	Asp	Ile	Tyr	Ser	Leu	Gly	Val	Val		
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ggc	tat	gag	atg	atg	gct	ggc	cgc	cgc	ccg	ttc	act	gga	gat	tct	tcg	787	
Gly	Tyr	Glu	Met	Met	Ala	Gly	Arg	Arg	Pro	Phe	Thr	Gly	Asp	Ser	Ser		
	215					220					225						
gtg	tct	gtg	gcg	atc	gcg	cac	atc	aac	caa	gct	ccg	ccg	cag	atg	ccc	835	
Val	Ser	Val	Ala	Ile	Ala	His	Ile	Asn	Gln	Ala	Pro	Pro	Gln	Met	Pro		
	230				235					240					245		
acc	agc	att	tcg	gca	cag	act	cgc	gag	ttg	att	ggc	att	gcg	ttg	cgc	883	
Thr	Ser	Ile	Ser	Ala	Gln	Thr	Arg	Glu	Leu	Ile	Gly	Ile	Ala	Leu	Arg		
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aag	gat	ccg	ggg	cgc	cgt	ttc	cct	gat	gga	aat	gaa	atg	gcg	cta	gct	931	
Lys	Asp	Pro	Gly	Arg	Arg	Phe	Pro	Asp	Gly	Asn	Glu	Met	Ala	Leu	Ala		

265	270	275	
gtt tct gct gtg cgc ctt ggc aag cgc ccg cct caa ccg cgc acg agc Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro Gln Pro Arg Thr Ser 280 285 290			979
gcg atg atg gcg cag gcg gag gcg ccg tcg cca agc gaa tca acg gcg Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro Ser Glu Ser Thr Ala 295 300 305			1027
atg ctg ggc agg gtg gcc cgg cct gca aca atc acc caa gaa gcg gcc Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile Thr Gln Glu Ala Ala 310 315 320 325			1075
ccg aaa cgc ggt tcc ggc att ggc att ggt ctg ttc atc gca gct ttg Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu Phe Ile Ala Ala Leu 330 335 340			1123
ctt gcc gtg att att ggc gcg gtg atc tat gcg ggc acc acc gga att Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala Gly Thr Thr Gly Ile 345 350 355			1171
ttg ttc aac gac act ccg gaa gaa acc acc aca cct gaa acc att acg Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr Pro Glu Thr Ile Thr 360 365 370			1219
gaa aca tac acc cca acc gtg gag gaa acc acc tct cag tgg gta ccg Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr Ser Gln Trp Val Pro 375 380 385			1267
cca acg cct cca aca cgg tca aca ttc acc gaa cct gaa aca act tca Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu Pro Glu Thr Thr Ser 390 395 400 405			1315
cac cgt ccg acg aca agt gaa gag agc aca tcc gag gaa cca acc acg His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser Glu Glu Pro Thr Thr 410 415 420			1363
gaa gct cca aca agt agc cga act gtg cct caa atc cct acc tct aca Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln Ile Pro Thr Ser Thr 425 430 435			1411
cct agg acg agt gct agc gtt cca gtt gag act aat gca ccg gct gat Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr Asn Ala Pro Ala Asp 440 445 450			1459
gat tta atc gac gcc gta aat ggc cta ttg gat gta gga gga gcg cag Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp Val Gly Gly Ala Gln 455 460 465			1507
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<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 20 25 30
 Thr Val Trp Leu Ala Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile
 35 40 45
 Lys Val Leu Arg Pro Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg
 50 55 60
 Phe Arg Asn Glu Ala Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val
 65 70 75 80
 Val Ala Thr Tyr Asp Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr
 85 90 95
 Phe Cys Phe Ile Val Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp
 100 105 110
 Leu Leu Glu Arg Glu Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val
 115 120 125
 Met Glu Gln Ala Ala His Gly Leu Ser Val Ile His Arg Met Asp Met
 130 135 140
 Val His Arg Asp Ile Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly
 145 150 155 160
 Ile Val Lys Ile Thr Asp Phe Gly Ile Ala Lys Ala Ala Ala Ala Val
 165 170 175
 Pro Leu Thr Arg Thr Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser
 180 185 190
 Pro Glu Gln Ala Gln Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr
 195 200 205
 Ser Leu Gly Val Val Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe
 210 215 220
 Thr Gly Asp Ser Ser Val Ser Val Ala Ile Ala His Ile Asn Gln Ala
 225 230 235 240
 Pro Pro Gln Met Pro Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile
 245 250 255
 Gly Ile Ala Leu Arg Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn
 260 265 270
 Glu Met Ala Leu Ala Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro
 275 280 285
 Gln Pro Arg Thr Ser Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro
 290 295 300
 Ser Glu Ser Thr Ala Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile
 305 310 315 320
 Thr Gln Glu Ala Ala Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu
 325 330 335

Phe Ile Ala Ala Leu Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala
 340 345 350
 Gly Thr Thr Gly Ile Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr
 355 360 365
 Pro Glu Thr Ile Thr Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr
 370 375 380
 Ser Gln Trp Val Pro Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu
 385 390 395 400
 Pro Glu Thr Thr Ser His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser
 405 410 415
 Glu Glu Pro Thr Thr Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln
 420 425 430
 Ile Pro Thr Ser Thr Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr
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 Val Gly Gly Ala Gln
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<210> 61
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1231)
 <223> RXA00813

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 Met Thr Asp Ile Asp
 1 5
 ctg gtg gtg gaa aac gtc caa agg att atc gcc acc aaa gag aca ccg 163
 Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala Thr Lys Glu Thr Pro
 10 15 20
 ccg acc tct gcg gaa ata gcg agc ctg att cgg gaa caa gca ggc gtg 211
 Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg Glu Gln Ala Gly Val
 25 30 35
 atc agt aac gag gac atc gtg atg gtg ttg cgt cga ctg cgc agt gat 259
 Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg Arg Leu Arg Ser Asp
 40 45 50
 tct gtg ggc gtg gga ccg ttg gaa tct ctg ctt gcg ctt cct ggc gtg 307
 Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu Ala Leu Pro Gly Val
 55 60 65

acg gat gtg ttg gtt aat gcc cat gac agc gtg tgg att gat cgc ggt	355
Thr Asp Val Leu Val Asn Ala His Asp Ser Val Trp Ile Asp Arg Gly	
70 75 80 85	
cag ggc gtg gag aaa gtc gac atg gat ctg ggc tca gag gag gcg gtg	403
Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly Ser Glu Glu Ala Val	
90 95 100	
cgt cgc ctt gcc acc cgg ttg gcg ttg acc tgt ggc aga cgc tta gat	451
Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys Gly Arg Arg Leu Asp	
105 110 115	
gat gcg cag cct ttc gct gat ggc cga atc acc agg gac gac ggc agc	499
Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr Arg Asp Asp Gly Ser	
120 125 130	
gtg ttg cgc att cac gcg gtg ttg gca ccc ttg gcg gaa tcc ggc acg	547
Val Leu Arg Ile His Ala Val Leu Ala Pro Leu Ala Glu Ser Gly Thr	
135 140 145	
tgc atc agt gtg cga gta ctg cgt caa gca cgg ctg agc ctt gat gat	595
Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg Leu Ser Leu Asp Asp	
150 155 160 165	
ctt atc caa agc ggc acg gtg cct gag gac atc gcg cct gcg ctc cgg	643
Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile Ala Pro Ala Leu Arg	
170 175 180	
aac atc atc aat caa cgg cgc tcg ttc ctt gtt gtc ggt ggc acc ggc	691
Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val Val Gly Gly Thr Gly	
185 190 195	
aca ggg aaa acc aca ttg ctg tcc gcg atg ctc acc gaa gtt ccc gct	739
Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu Thr Glu Val Pro Ala	
200 205 210	
gat caa cga atc atc tgc atc gag gac acc gca gag ctt cat ccc ggc	787
Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala Glu Leu His Pro Gly	
215 220 225	
cat cca agc acc atc aac ttg gtg tct cgc caa gca aac gtc gag ggc	835
His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln Ala Asn Val Glu Gly	
230 235 240 245	
gcc ggc gcc gtg agc atg gcg gat ttg ttg aaa caa tcg ctg cgc atg	883
Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys Gln Ser Leu Arg Met	
250 255 260	
agg cct gac cgg att gtc gtc gga gag att cgc ggt gcg gaa gtc gtg	931
Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg Gly Ala Glu Val Val	
265 270 275	
gat ctt ttg gct gcg atg aat acc gga cac gac ggc ggt gct ggc acc	979
Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp Gly Gly Ala Gly Thr	
280 285 290	
att cac gcg aac tcc atc tct gaa gtt ccc gcg cgc atg gaa gct ctt	1027
Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala Arg Met Glu Ala Leu	
295 300 305	
gcg gcg acc ggc gga ttg gac cgc atg gca ttg cat tct caa ctc gcg	1075

Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu His Ser Gln Leu Ala
 310 315 320 325

gcc gca gtg gac att gtg ctg gtc atg aaa cac acc cct ttt ggc cgc 1123
 Ala Ala Val Asp Ile Val Leu Val Met Lys His Thr Pro Phe Gly Arg
 330 335 340

agg cta gct caa ctc ggg gtg ctc cgc gga aat cct gtg acc acg cag 1171
 Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn Pro Val Thr Thr Gln
 345 350 355

gtg gtg tgg gat ttg gac cac ggc atg cac gaa ggg agc gaa gag gca 1219
 Val Val Trp Asp Leu Asp His Gly Met His Glu Gly Ser Glu Glu Ala
 360 365 370

tgg ttt atg ccc taggccttct tagcgtggcg gtg 1254
 Trp Phe Met Pro
 375

<210> 62

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

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Thr Lys Glu Thr Pro Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg
 20 25 30

Glu Gln Ala Gly Val Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg
 35 40 45

Arg Leu Arg Ser Asp Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu
 50 55 60

Ala Leu Pro Gly Val Thr Asp Val Leu Val Asn Ala His Asp Ser Val
 65 70 75 80

Trp Ile Asp Arg Gly Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly
 85 90 95

Ser Glu Glu Ala Val Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys
 100 105 110

Gly Arg Arg Leu Asp Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr
 115 120 125

Arg Asp Asp Gly Ser Val Leu Arg Ile His Ala Val Leu Ala Pro Leu
 130 135 140

Ala Glu Ser Gly Thr Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg
 145 150 155 160

Leu Ser Leu Asp Asp Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile
 165 170 175

Ala Pro Ala Leu Arg Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val
 180 185 190

Val Gly Gly Thr Gly Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu
 195 200 205
 Thr Glu Val Pro Ala Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala
 210 215 220
 Glu Leu His Pro Gly His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln
 225 230 235 240
 Ala Asn Val Glu Gly Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys
 245 250 255
 Gln Ser Leu Arg Met Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg
 260 265 270
 Gly Ala Glu Val Val Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp
 275 280 285
 Gly Gly Ala Gly Thr Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala
 290 295 300
 Arg Met Glu Ala Leu Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu
 305 310 315 320
 His Ser Gln Leu Ala Ala Ala Val Asp Ile Val Leu Val Met Lys His
 325 330 335
 Thr Pro Phe Gly Arg Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn
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 Pro Val Thr Thr Gln Val Val Trp Asp Leu Asp His Gly Met His Glu
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 Gly Ser Glu Glu Ala Trp Phe Met Pro
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<210> 63
 <211> 2061
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2038)
 <223> RXA01826

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 Val Thr Phe Val Ile
 1 5
 gct gat cgc tat gaa ctg gat gcc gtc atc ggc tcc ggt ggc atg agc 163
 Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly Ser Gly Gly Met Ser
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 gag gtg ttc gcg gcc acc gac acg ctc att ggt cgg gag gtc gcg gta 211
 Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly Arg Glu Val Ala Val

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Lys	Met	Leu	Arg	Ile	Asp	Leu	Ala	Lys	Asp	Pro	Asn	Phe	Arg	Glu	Arg					
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Phe	Arg	Arg	Glu	Ala	Gln	Asn	Ser	Gly	Arg	Leu	Ser	His	Ser	Ser	Ile					
	55					60					65									
gtc	gct	gtt	ttt	gac	acc	ggc	gaa	gta	gac	aaa	gac	ggc	acc	tct	gtt	355				
Val	Ala	Val	Phe	Asp	Thr	Gly	Glu	Val	Asp	Lys	Asp	Gly	Thr	Ser	Val					
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Pro	Tyr	Ile	Val	Met	Glu	Arg	Val	Gln	Gly	Arg	Asn	Leu	Arg	Glu	Val					
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gtc	acc	gaa	gac	ggc	gta	ttc	acc	cca	gtt	gag	gca	gcc	aac	atc	ctc	451				
Val	Thr	Glu	Asp	Gly	Val	Phe	Thr	Pro	Val	Glu	Ala	Ala	Asn	Ile	Leu					
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atc	cct	gtg	tgt	gaa	gcg	ctg	cag	gca	tcc	cat	gac	gcc	ggc	att	att	499				
Ile	Pro	Val	Cys	Glu	Ala	Leu	Gln	Ala	Ser	His	Asp	Ala	Gly	Ile	Ile					
		120					125					130								
cac	cgc	gat	gtg	aaa	ccc	gcc	aac	atc	atg	atc	acc	aac	acc	ggc	ggc	547				
His	Arg	Asp	Val	Lys	Pro	Ala	Asn	Ile	Met	Ile	Thr	Asn	Thr	Gly	Gly					
	135					140					145									
gtg	aaa	gtc	atg	gac	ttc	ggc	atc	gcc	cgc	gcg	gtc	aac	gat	tcc	acc	595				
Val	Lys	Val	Met	Asp	Phe	Gly	Ile	Ala	Arg	Ala	Val	Asn	Asp	Ser	Thr					
	150				155				160						165					
tcc	gcc	atg	act	caa	acc	tcc	gca	gtc	atc	ggc	acc	gcc	cag	tac	ctc	643				
Ser	Ala	Met	Thr	Gln	Thr	Ser	Ala	Val	Ile	Gly	Thr	Ala	Gln	Tyr	Leu					
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tcc	cct	gag	cag	gcc	cgc	ggc	aaa	ccc	gcc	gat	gcg	cgt	tcc	gat	att	691				
Ser	Pro	Glu	Gln	Ala	Arg	Gly	Lys	Pro	Ala	Asp	Ala	Arg	Ser	Asp	Ile					
			185				190						195							
tac	gcc	acc	ggc	tgc	gtc	atg	tac	gaa	tta	gtc	acc	ggc	aag	cca	cct	739				
Tyr	Ala	Thr	Gly	Cys	Val	Met	Tyr	Glu	Leu	Val	Thr	Gly	Lys	Pro	Pro					
		200					205					210								
ttt	gaa	ggc	gag	tcc	cct	ttc	gcc	gtg	gcc	tac	caa	cac	gtc	cag	gaa	787				
Phe	Glu	Gly	Glu	Ser	Pro	Phe	Ala	Val	Ala	Tyr	Gln	His	Val	Gln	Glu					
	215					220					225									
gac	ccc	acc	cct	cct	tcg	gat	ttc	atc	gcg	gac	ctc	acc	ccg	acc	tct	835				
Asp	Pro	Thr	Pro	Pro	Ser	Asp	Phe	Ile	Ala	Asp	Leu	Thr	Pro	Thr	Ser					
	230				235					240					245					
gct	gtc	aac	gtg	gat	gcc	gtg	gta	ctc	acc	gcc	atg	gca	aaa	cac	ccc	883				
Ala	Val	Asn	Val	Asp	Ala	Val	Val	Leu	Thr	Ala	Met	Ala	Lys	His	Pro					
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gcc	gac	cgc	tac	caa	aca	gcc	tcc	gaa	atg	gcc	gct	gac	ctg	ggc	cgg	931				
Ala	Asp	Arg	Tyr	Gln	Thr	Ala	Ser	Glu	Met	Ala	Ala	Asp	Leu	Gly	Arg					
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cta tcc cgc aat gca gtc tcc cat gcc gca cgc gcg cat gta gaa aca	979
Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg Ala His Val Glu Thr	
280 285 290	
gaa gaa acc cca gaa gag ccc gaa act cgc ttc tcg acg cgc acc tcc	1027
Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe Ser Thr Arg Thr Ser	
295 300 305	
acc caa gtg gcc ccc gcc gca ggc gtg gct gcg gcc agt acg ggg tca	1075
Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala Ala Ser Thr Gly Ser	
310 315 320 325	
ggg tct tct tcg cgt aaa cgt gga tcc aga ggc ctc acc gcc ctg gcc	1123
Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly Leu Thr Ala Leu Ala	
330 335 340	
atc gtg tta tcc cta ggt gtc gtc ggc gtt gcc ggt gcc ttc acc tac	1171
Ile Val Leu Ser Leu Gly Val Val Gly Val Ala Gly Ala Phe Thr Tyr	
345 350 355	
gac tac ttt gcc aac agc tcc tcc act gca acc agc gcg atc ccc aat	1219
Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr Ser Ala Ile Pro Asn	
360 365 370	
gtg gaa ggc ctc ccg cag caa gaa gct ctc aca gaa ctt caa gca gca	1267
Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr Glu Leu Gln Ala Ala	
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Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser Ala Asp Val Ala Glu	
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Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly Ser Glu Ile Arg Gln	
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Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly Arg Glu Met Ile Asn	
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Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp Ala Ala Arg Ala Leu	
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Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val Arg Glu Glu Thr Ser	
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Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln Asn Pro Glu Ala Gly	
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Gln Glu Val Val Val Gly Ser Ser Val Ser Leu Thr Met Ser Ser Gly	
490 495 500	
acc gag agc atc cga gtg ccc aac ctc acc ggc atg aac tgg tca caa	1651
Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly Met Asn Trp Ser Gln	
505 510 515	

gca gaa caa aac ctc atc tcc atg ggc ttt aac ccc aca gct tcc tac 1699
 Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn Pro Thr Ala Ser Tyr
 520 525 530

tta gac agc agc gaa cca gaa ggc gaa gtc ctc tca gtt tcc agc caa 1747
 Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu Ser Val Ser Ser Gln
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 Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr Val Glu Val Ser Asn
 550 555 560 565

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 Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg Met Ser Thr Glu Gln
 570 575 580

gcc atc agt gcc ctc cgc gct gct ggc tgg acc gcc cca gat caa tcc 1891
 Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr Ala Pro Asp Gln Ser
 585 590 595

ctg atc gtc ggc gac ccc atc cac acc gca gcc ctc gtg gat caa aac 1939
 Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala Leu Val Asp Gln Asn
 600 605 610

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gcc caa gtg caa gtg cga ctc ttc gaa ttc gat ctc gct gca ctc gtg 2035
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Ser His Ser Ser Ile Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys
 65 70 75 80

Asp Gly Thr Ser Val Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg
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 Thr Asn Thr Gly Gly Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala
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 Val Asn Asp Ser Thr Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly
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 180 185 190
 Ala Arg Ser Asp Ile Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val
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 Thr Gly Lys Pro Pro Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr
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 Met Ala Lys His Pro Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala
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 Ala Asp Leu Gly Arg Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg
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 Ala His Val Glu Thr Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe
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 Ser Thr Arg Thr Ser Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala
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 Ala Ser Thr Gly Ser Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly
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 Gly Ala Phe Thr Tyr Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr
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 Glu Leu Gln Ala Ala Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser
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 Ala Asp Val Ala Glu Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly
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 Ser Glu Ile Arg Gln Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly

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Arg Glu Glu Thr Ser Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln 465 470 475 480		
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Thr Met Ser Ser Gly Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly 500 505 510		
Met Asn Trp Ser Gln Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn 515 520 525		
Pro Thr Ala Ser Tyr Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu 530 535 540		
Ser Val Ser Ser Gln Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr 545 550 555 560		
Val Glu Val Ser Asn Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg 565 570 575		
Met Ser Thr Glu Gln Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr 580 585 590		
Ala Pro Asp Gln Ser Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala 595 600 605		
Leu Val Asp Gln Asn Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr 610 615 620		
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 Met Ser Thr Val Tyr
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Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met Ala Leu Lys Val Met	
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Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg Gln Arg Ser Arg Arg	
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Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro Asn Leu Val Asn Val	
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Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr Leu Val Met Glu Leu	
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atc act ggt ggc acc ttg cgt gag ttg ctg gct gag cgg gga cct atg	355
Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala Glu Arg Gly Pro Met	
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ccc ccg cat gct gct gtg ggc gtt atg cgt ggg gtg ctc acg ggt ctc	403
Pro Pro His Ala Ala Val Gly Val Met Arg Gly Val Leu Thr Gly Leu	
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gcg gct gcc cac ccg gcg ggc atg gtg cac ccg gat atc aag cct gac	451
Ala Ala Ala His Arg Ala Gly Met Val His Arg Asp Ile Lys Pro Asp	
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aac gtg ttg atc aat agt gat cac cag gtg aaa ctg tct gat ttc ggc	499
Asn Val Leu Ile Asn Ser Asp His Gln Val Lys Leu Ser Asp Phe Gly	
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ttg gtt cga gcg gct cac gcc ggc cag tct cag gac aat cag att gtg	547
Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln Asp Asn Gln Ile Val	
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Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val Glu Gly Gly Glu Ile	
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Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile Val Leu Phe Glu Leu	
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Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp Asp Leu Asp His Ala	
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Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro Ser Ser Leu Ile Asp	
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Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala Thr Ala Thr Ser Ile	
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Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu Phe Leu Ser Ala Leu	
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Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala Phe Arg Val Pro Val	
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Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala Gln Val Pro Asp Ala	
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cag cca act gat atg ttt acc acc cat atc ccc aag act cct gag cct	979
Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro Lys Thr Pro Glu Pro	
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Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala Asn Glu Thr Ser Ile	
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Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala Gln Asn Pro Leu Gln	
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Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro Asp Thr Ala Leu	
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Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp Glu Pro Glu Ile Asn	
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Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr Leu Trp Ser Ile Phe	
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Val Val Ala Val Ile Ala Ala Val Ala Val Gly Gly Trp Trp Phe Gly	
375 380 385	
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Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu Gly Met Asp Glu Val	
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Gln Ala Val Ala Val Glu Glu Ala Gly Phe Val Ala Val Ala Glu	
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Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser Ile Ile Gly Thr Glu	
425 430 435	
cct tct ttt ggt gag cgc ctt cct cgc ggc gag gat gtt tct gtc ctc	1459
Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu Asp Val Ser Val Leu	
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Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu Ser Glu Asp Arg Ser	
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tta agc acc gtt cgt gaa gag ttg gaa cag cgc acg ttc gtc tgg gtt	1555
Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg Thr Phe Val Trp Val	
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Ser	Phe	Thr	Pro	Ser	Ser	Gly	Thr	Gln	Leu	Asp	Val	Gly	Glu	Thr	Val		
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Gln	Ile	His	Leu	Ser	Arg	Gly	Pro	Ala	Pro	Val	Glu	Ile	Pro	Asp	Val		
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tct	ggc	atg	gga	gtg	gat	cag	gca	aca	cgt	gtg	ttg	gag	cgc	gca	ggg	1747	
Ser	Gly	Met	Gly	Val	Asp	Gln	Ala	Thr	Arg	Val	Leu	Glu	Arg	Ala	Gly		
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Leu	Ser	Val	Glu	Arg	Thr	Glu	Glu	Gly	Phe	Asp	Ala	Glu	Thr	Pro	Asn		
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Gly	Asp	Val	Tyr	Gly	Thr	Ser	Pro	Lys	Val	Ser	Thr	Glu	Val	Lys	Arg		
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Gly	Thr	Ser	Val	Val	Leu	Gln	Val	Ser	Asn	Ala	Ile	Ser	Val	Pro	Asp		
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Val	Val	Gly	Met	Thr	Lys	Asp	Glu	Ala	Thr	Ala	Ala	Leu	Ala	Glu	Glu		
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Ser	Ala	Asp	Ala	Val	Val	Thr	Val	Glu	Pro	Glu	Ser	Gly	Ser	Arg	Val		
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gat	cca	gcg	cat	ccg	cag	gtc	agc	ctc	ggg	tta	gct	ggg	gag	att	caa	2083	
Asp	Pro	Ala	His	Pro	Gln	Val	Ser	Leu	Gly	Leu	Ala	Gly	Glu	Ile	Gln		
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gtt	cca	agc	gtg	gtt	gga	cgt	aag	gtt	agc	gat	gct	cga	agc	att	ctg	2131	
Val	Pro	Ser	Val	Val	Gly	Arg	Lys	Val	Ser	Asp	Ala	Arg	Ser	Ile	Leu		
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Glu	Glu	Ala	Gly	Leu	Thr	Leu	Thr	Thr	Asp	Ala	Asp	Asp	Asn	Asp	Arg		
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Ile	Tyr	Ser	Gln	Thr	Pro	Arg	Ala	Arg	Ser	Glu	Val	Ser	Val	Gly	Gly		
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<213> Corynebacterium glutamicum

<400> 66

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Glu	Arg	Gly	Pro	Met	Pro	Pro	His	Ala	Ala	Val	Gly	Val	Met	Arg	Gly
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Val	Leu	Thr	Gly	Leu	Ala	Ala	Ala	His	Arg	Ala	Gly	Met	Val	His	Arg
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Asp	Ile	Lys	Pro	Asp	Asn	Val	Leu	Ile	Asn	Ser	Asp	His	Gln	Val	Lys
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Leu	Ser	Asp	Phe	Gly	Leu	Val	Arg	Ala	Ala	His	Ala	Gly	Gln	Ser	Gln
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Asp	Asn	Gln	Ile	Val	Gly	Thr	Val	Ala	Tyr	Leu	Ser	Pro	Glu	Gln	Val
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Glu	Gly	Gly	Glu	Ile	Gly	Pro	Ala	Ser	Asp	Val	Tyr	Ser	Ala	Gly	Ile
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Val	Leu	Phe	Glu	Leu	Leu	Thr	Gly	Thr	Thr	Pro	Phe	Ser	Gly	Glu	Asp
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Asp	Leu	Asp	His	Ala	Tyr	Ala	Arg	Leu	Thr	Glu	Val	Val	Pro	Ala	Pro
		195					200					205			

Ser	Ser	Leu	Ile	Asp	Gly	Val	Pro	Ser	Leu	Ile	Asp	Glu	Leu	Val	Ala
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Thr	Ala	Thr	Ser	Ile	Asn	Pro	Glu	Asp	Arg	Phe	Asp	Asp	Ser	Gly	Glu
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Phe	Leu	Ser	Ala	Leu	Glu	Asp	Val	Ala	Thr	Glu	Leu	Ser	Leu	Pro	Ala
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Phe	Arg	Val	Pro	Val	Pro	Val	Asn	Ser	Ala	Ala	Asn	Arg	Ala	Asn	Ala
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Gln	Val	Pro	Asp	Ala	Gln	Pro	Thr	Asp	Met	Phe	Thr	Thr	His	Ile	Pro
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Lys	Thr	Pro	Glu	Pro	Asp	His	Thr	Ala	Ile	Ile	Pro	Val	Ala	Ser	Ala
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 Pro Asp Thr Ala Leu Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp
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 Glu Pro Glu Ile Asn Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr
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 Leu Trp Ser Ile Phe Val Val Ala Val Ile Ala Ala Val Ala Val Gly
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 Ile Ile Gly Thr Glu Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu
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 Ala Gly Glu Ile Gln Val Pro Ser Val Val Gly Arg Lys Val Ser Asp
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 Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu Asp Asn Val Ile Phe 20
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 Ser Ser Cys Gly Met Gly Asn Trp His Val Gly Gln Pro Ala Asp Lys 35
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 cga gct ctc gcg gaa ctg aaa tca gcc ggt tac aac ggc gac acc cac 259
 Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr Asn Gly Asp Thr His 50
 40 45
 cgc gca gca caa ctt ggt ccc gag cac atg cgc gca gat ctc ttc gtc 307
 Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg Ala Asp Leu Phe Val 65
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 gcg cta gat tcc ggc cac gcc ggt gag ctc gcc gca acg ggt gtt ccc 355
 Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala Ala Thr Gly Val Pro 85
 70 75 80
 aac gac aaa atc cgc ctc atg cgt tcc ttc gac cca gag tcc aac ccc 403
 Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp Pro Glu Ser Asn Pro 100
 90 95
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Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr Ser Gln Asp Phe Val
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
 Met Ser Glu Val Ile Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu
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Asp Asn Val Ile Phe Ser Ser Cys Gly Met Gly Asn Trp His Val Gly
 20 25 30

Gln Pro Ala Asp Lys Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr
 35 40 45

Asn Gly Asp Thr His Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg
 50 55 60

Ala Asp Leu Phe Val Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala
 65 70 75 80

Ala Thr Gly Val Pro Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp
 85 90 95

Pro Glu Ser Asn Pro Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr
 100 105 110

Ser Gln Asp Phe Val Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro
 115 120 125

Gly Leu Leu Glu Trp Val Arg Asp His Ile Arg Thr Asp Ser
 130 135 140

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 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(703)
 <223> RXA01272

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                                         Met Ser Asn Ser Phe
                                         1                               5

act att ctc act gtc tgt act gga aac att tgc cgc tcc ccg tta gct 163
Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys Arg Ser Pro Leu Ala
                        10                               15                               20

aag cag cta ctt gaa ctt gag ctt ccg ggg gca gat ata atc cgc gtt 211
Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala Asp Ile Ile Arg Val
                        25                               30                               35

gat tcc gcc ggt gtt cag gcg atg gtt gat tcg cct atg ccg gag caa 259
Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser Pro Met Pro Glu Gln
                        40                               45                               50

tct tta gaa atc gca cgt aaa cag ggc ata gaa aac cct gag gag cac 307
Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu Asn Pro Glu Glu His
                        55                               60                               65

cga gct aag cag att act gag gag ctt gta aac caa tct gat ctg att 355
Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn Gln Ser Asp Leu Ile
                        70                               75                               80                               85

ctt gcg atg gat ccg ggg cat cga aaa tcc att gtc cag cta agc ccg 403
Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile Val Gln Leu Ser Pro
                        90                               95                               100

cgt gca acc cgt aag gtt ttc act gtt gtt gat ctt gcc agg tta att 451
Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp Leu Ala Arg Leu Ile
                        105                               110                               115

gag gca aca act gat gct gat ctg cag gaa gag ctc aat ctg gca ggg 499
Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu Leu Asn Leu Ala Gly
                        120                               125                               130

gat tcc gtg atc gat agg ctg cat gcg aca gtt gag gct gct cgt ctt 547
Asp Ser Val Ile Asp Arg Leu His Ala Thr Val Glu Ala Ala Arg Leu
                        135                               140                               145

agc cgc agt gaa ttg aat cct ctg gat aac ctc gca gat gaa gat att 595
Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu Ala Asp Glu Asp Ile
                        150                               155                               160                               165

gtt gac ccg tac gga aag agt caa tcg gtt tat gag gca tcg gcg agt 643
Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr Glu Ala Ser Ala Ser
                        170                               175                               180

cag cta att cca gct att cgt ttg att gct tct tat ttg aac aaa gca 691
Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser Tyr Leu Asn Lys Ala
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Leu Glu Ser Ala
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<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Asp Ile Ile Arg Val Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser
 35 40 45

Pro Met Pro Glu Gln Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu
 50 55 60

Asn Pro Glu Glu His Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn
 65 70 75 80

Gln Ser Asp Leu Ile Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile
 85 90 95

Val Gln Leu Ser Pro Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp
 100 105 110

Leu Ala Arg Leu Ile Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu
 115 120 125

Leu Asn Leu Ala Gly Asp Ser Val Ile Asp Arg Leu His Ala Thr Val
 130 135 140

Glu Ala Ala Arg Leu Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu
 145 150 155 160

Ala Asp Glu Asp Ile Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr
 165 170 175

Glu Ala Ser Ala Ser Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser
 180 185 190

Tyr Leu Asn Lys Ala Leu Glu Ser Ala
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<210> 71

<211> 1476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1453)

<223> RXA01830

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atatccgtat tggtcgtaca gcagtgaggc ttgttcctg atg ttg aaa ctt aaa 115
 Met Leu Lys Leu Lys
 1 5

tat gcg gtg gca tct gac cga ggg tta gtg cgc ggg aac aat gag gat 163
 Tyr Ala Val Ala Ser Asp Arg Gly Leu Val Arg Gly Asn Asn Glu Asp

				10				15				20				
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Ser	Ala	Tyr	Ala	Gly	Pro	His	Leu	Leu	Ala	Leu	Ala	Asp	Gly	Met	Gly	
25				30				35								
ggc	cat	gct	gct	ggt	gag	atc	gct	tcc	caa	acc	atg	atc	aac	cat	ttg	259
Gly	His	Ala	Ala	Gly	Glu	Ile	Ala	Ser	Gln	Thr	Met	Ile	Asn	His	Leu	
40				45				50								
cgt	gcg	ctt	gat	gtt	gat	cct	ggt	gat	aac	gat	atg	ttg	gcg	ctg	gtg	307
Arg	Ala	Leu	Asp	Val	Asp	Pro	Gly	Asp	Asn	Asp	Met	Leu	Ala	Leu	Val	
55				60				65								
ggc	atg	gtg	gca	ggc	gaa	gcc	aac	gcg	gcg	att	gct	gag	ggc	atc	gcc	355
Gly	Met	Val	Ala	Gly	Glu	Ala	Asn	Ala	Ala	Ile	Ala	Glu	Gly	Ile	Ala	
70				75				80				85				
gaa	gac	ccg	gcg	cgc	gac	ggc	atg	ggc	act	acg	ttg	acg	gcg	ttc	atg	403
Glu	Asp	Pro	Ala	Arg	Asp	Gly	Met	Gly	Thr	Thr	Leu	Thr	Ala	Phe	Met	
90				95				100								
ttt	aac	ggg	cgt	gac	ctg	gca	atg	tgc	cac	gtc	ggc	gat	agt	cgt	ggt	451
Phe	Asn	Gly	Arg	Asp	Leu	Ala	Met	Cys	His	Val	Gly	Asp	Ser	Arg	Gly	
105				110				115								
tat	gtg	ctt	cgc	gac	gat	aag	ttg	gta	cag	gtt	aca	gtc	gac	gat	act	499
Tyr	Val	Leu	Arg	Asp	Asp	Lys	Leu	Val	Gln	Val	Thr	Val	Asp	Asp	Thr	
120				125				130								
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Phe	Val	Gln	Ser	Leu	Val	Ala	Glu	Gly	Lys	Leu	Asp	Pro	Glu	Asp	Val	
135				140				145								
tca	act	cac	cct	cag	cgt	tct	ttg	att	ctg	aag	gct	tac	acc	ggc	cat	595
Ser	Thr	His	Pro	Gln	Arg	Ser	Leu	Ile	Leu	Lys	Ala	Tyr	Thr	Gly	His	
150				155				160				165				
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Pro	Val	Glu	Pro	Thr	Leu	Glu	Gln	Phe	Pro	Ala	Leu	Pro	Gly	Asp	Arg	
170				175				180								
ttg	ttg	ttg	tgc	tct	gat	ggt	cta	tca	gat	ccg	gtt	aca	cac	tcc	acg	691
Leu	Leu	Leu	Cys	Ser	Asp	Gly	Leu	Ser	Asp	Pro	Val	Thr	His	Ser	Thr	
185				190				195								
att	gaa	gaa	aca	gtg	cgt	gta	ggc	acc	ccg	cag	gat	gcg	tcc	acc	aag	739
Ile	Glu	Glu	Thr	Val	Arg	Val	Gly	Thr	Pro	Gln	Asp	Ala	Ser	Thr	Lys	
200				205				210								
ttg	gtg	gag	ttg	gcg	ctg	cgt	tct	ggc	ggt	ccg	gac	aat	gtg	acg	gtc	787
Leu	Val	Glu	Leu	Ala	Leu	Arg	Ser	Gly	Gly	Pro	Asp	Asn	Val	Thr	Val	
215				220				225								
att	gtg	gcc	gat	gtt	gta	gaa	gtc	acc	gag	gcg	gaa	gca	gca	gcg	gaa	835
Ile	Val	Ala	Asp	Val	Val	Glu	Val	Thr	Glu	Ala	Glu	Ala	Ala			

gat ccg cgg cct gat acc gct gcg gga cgc gct gcg gcg atc aca cgg 931
Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala Ala Ala Ile Thr Arg
265 270 275

cga gct caa gtg att gat ccg gca cca aag ata tct gat gct gga acg 979
Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile Ser Asp Ala Gly Thr
280 285 290

gag gat att ccc aca att gag gag cca cca gag aaa agt tcc agc aaa 1027
Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu Lys Ser Ser Ser Lys
295 300 305

ctt gcg gta ttg atc gta gcc ctg gtc atc ctc atc ggt gta gtt gcc 1075
Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu Ile Gly Val Val Ala
310 315 320 325

gca gga tgg tgg ggc tac tcc cgt att gac agc act ttt tac gtc gcg 1123
Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser Thr Phe Tyr Val Ala
330 335 340

gtc aat gat gag gaa gcc atc acc gtg gaa cac ggt gtg gat tac cgc 1171
Val Asn Asp Glu Glu Ala Ile Thr Val Glu His Gly Val Asp Tyr Arg
345 350 355

atc ttt ggc aag gat tta cat tcg caa ttc cag gtg gcg tgc ctg aat 1219
Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln Val Ala Cys Leu Asn
360 365 370

gaa gct ggc acc ttg tca ctc aag gaa tcc tgt gaa aac ggt acg tct 1267
Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys Glu Asn Gly Thr Ser
375 380 385

ttc aaa ttg gat gat tta ccg gca tct gtt cgc ggt agt gtc gca gga 1315
Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg Gly Ser Val Ala Gly
390 395 400 405

tta ccg tct ggg tcg tat gac gag gtc cag gcg caa atg caa cgg ctg 1363
Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala Gln Met Gln Arg Leu
410 415 420

gct gct caa gct ttg cca gtg tgc gtg aac tta gaa gta aca acc ggt 1411
Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu Glu Val Thr Thr Gly
425 430 435

ggc gat aga aac gaa ccc gga gtc aat tgt agg gag gtc tca 1453
Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg Glu Val Ser
440 445 450

tgaacacgct tgaacgatta aag 1476

<210> 72

<211> 451

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Gly Asn Asn Glu Asp Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu
 20 25 30
 Ala Asp Gly Met Gly Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr
 35 40 45
 Met Ile Asn His Leu Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp
 50 55 60
 Met Leu Ala Leu Val Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile
 65 70 75 80
 Ala Glu Gly Ile Ala Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr
 85 90 95
 Leu Thr Ala Phe Met Phe Asn Gly Arg Asp Leu Ala Met Cys His Val
 100 105 110
 Gly Asp Ser Arg Gly Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val
 115 120 125
 Thr Val Asp Asp Thr Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu
 130 135 140
 Asp Pro Glu Asp Val Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys
 145 150 155 160
 Ala Tyr Thr Gly His Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala
 165 170 175
 Leu Pro Gly Asp Arg Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro
 180 185 190
 Val Thr His Ser Thr Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln
 195 200 205
 Asp Ala Ser Thr Lys Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro
 210 215 220
 Asp Asn Val Thr Val Ile Val Ala Asp Val Val Glu Val Thr Glu Ala
 225 230 235 240
 Glu Ala Ala Ala Glu Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn
 245 250 255
 Gly Glu Gln Pro Glu Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala
 260 265 270
 Ala Ala Ile Thr Arg Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile
 275 280 285
 Ser Asp Ala Gly Thr Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu
 290 295 300
 Lys Ser Ser Ser Lys Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu
 305 310 315 320
 Ile Gly Val Val Ala Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser
 325 330 335
 Thr Phe Tyr Val Ala Val Asn Asp Glu Glu Ala Ile Thr Val Glu His

340		345		350
Gly Val Asp Tyr Arg Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln				
355		360		365
Val Ala Cys Leu Asn Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys				
370		375		380
Glu Asn Gly Thr Ser Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg				
385		390		395
Gly Ser Val Ala Gly Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala				
	405		410	415
Gln Met Gln Arg Leu Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu				
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Glu Val Thr Thr Gly Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg				
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Glu Val Ser				
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<210> 73
 <211> 2199
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2176)
 <223> RXA02747

<400> 73
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 Met Asn Asn Pro Ala
 1 5
 cag ctg cgc caa gat act gaa aag gaa gtc ctg gcg ttg ctg ggc tct 163
 Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu Ala Leu Leu Gly Ser
 10 15 20
 ttg gtt tta ccc gcc ggc acc gcg ctt gcc gcc acc gga tct ttg gcc 211
 Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala Thr Gly Ser Leu Ala
 25 30 35
 agg tcc gaa ctc acg ccg tat tcc gat ttg gac ctc att ttg atc cat 259
 Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp Leu Ile Leu Ile His
 40 45 50
 cca cca gga gcc acc ccg gat ggc gtg gag gat ttg tgg tac ccg att 307
 Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp Leu Trp Tyr Pro Ile
 55 60 65
 tgg gac gca aaa aag cgt ctc gac tac tcc gtg cgc acc cca gat gag 355
 Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val Arg Thr Pro Asp Glu
 70 75 80 85

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Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala	Ala	Leu	Ala	Met	Leu	
				90					95					100		
gac	ctg	cgg	ttt	gtc	gct	ggc	gat	gag	gat	ctg	tgt	gcc	aaa	acg	cgc	451
Asp	Leu	Arg	Phe	Val	Ala	Gly	Asp	Glu	Asp	Leu	Cys	Ala	Lys	Thr	Arg	
			105					110					115			
cgg	cgc	atc	gtg	gag	aag	tgg	cgc	cag	gaa	ctc	aac	aaa	aac	ttc	gat	499
Arg	Arg	Ile	Val	Glu	Lys	Trp	Arg	Gln	Glu	Leu	Asn	Lys	Asn	Phe	Asp	
		120					125					130				
gcc	gtt	gtg	gac	acc	gcg	att	gcc	cgt	tgg	cgc	cgc	tcc	gga	ccc	gtc	547
Ala	Val	Val	Asp	Thr	Ala	Ile	Ala	Arg	Trp	Arg	Arg	Ser	Gly	Pro	Val	
	135					140					145					
gtg	gca	atg	acg	cgg	cca	gat	ctt	aaa	cac	ggc	agg	gga	ggg	ctg	cgc	595
Val	Ala	Met	Thr	Arg	Pro	Asp	Leu	Lys	His	Gly	Arg	Gly	Gly	Leu	Arg	
150					155					160					165	
gat	ttc	gaa	ctg	atc	aag	gcc	ctc	gcg	ctc	ggc	cac	cta	tgc	aac	ctt	643
Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly	His	Leu	Cys	Asn	Leu	
				170					175					180		
cca	cag	ctt	gat	gcg	caa	cac	cag	ctg	ctt	ctc	gac	gcc	cgc	acc	ttg	691
Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu	Asp	Ala	Arg	Thr	Leu	
			185					190					195			
ctg	cac	gtc	cac	gcg	cga	cgc	tcc	cgc	gac	gtc	ctt	gac	ccc	gaa	ttt	739
Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val	Leu	Asp	Pro	Glu	Phe	
		200					205					210				
gcg	gtg	gat	gtg	gcc	atg	gat	ttg	ggc	ttt	gtt	gac	cgc	tat	cac	ctg	787
Ala	Val	Asp	Val	Ala	Met	Asp	Leu	Gly	Phe	Val	Asp	Arg	Tyr	His	Leu	
	215					220					225					
ggc	cgg	gag	atc	gcc	gat	gca	gcc	cgc	gcc	att	gat	gat	ggc	ctg	acc	835
Gly	Arg	Glu	Ile	Ala	Asp	Ala	Ala	Arg	Ala	Ile	Asp	Asp	Gly	Leu	Thr	
230					235					240					245	
acc	gcg	ctg	gcc	acc	gcc	cgt	ggc	att	ttg	cca	cgt	cgc	aca	ggt	ttt	883
Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro	Arg	Arg	Thr	Gly	Phe	
				250					255					260		
gca	ttc	agg	aat	gct	tct	cga	cgc	cca	ctt	gat	ctt	gat	gtc	gtc	gac	931
Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp	Leu	Asp	Val	Val	Asp	
			265					270					275			
gcc	aac	ggc	acc	atc	gaa	ttg	tcc	aaa	aaa	cca	gat	ctt	aat	gat	ccc	979
Ala	Asn	Gly	Thr	Ile	Glu	Leu	Ser	Lys	Lys	Pro	Asp	Leu	Asn	Asp	Pro	
		280					285					290				
gca	ctt	cca	ctt	cga	gtg	gcc	gca	gcc	gca	gca	acc	acc	gga	ctt	ccg	1027
Ala	Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Gly	Leu	Pro	
	295					300					305					
gtg	gca	gaa	tca	acc	tgg	gtt	cga	ctt	aat	gaa	tgc	ccg	cca	ctt	cct	1075
Val	Ala	Glu	Ser	Thr	Trp	Val	Arg	Leu	Asn	Glu	Cys	Pro	Pro	Leu	Pro	
310					315					320					325	
gag	cca	tgg	cct	gcc	aat	gca	gca	ggg	gac	ttc	ttt	cgg	att	ctc	tcc	1123

Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe	Phe	Arg	Ile	Leu	Ser		
				330					335					340			
agt	ccg	aaa	aac	tca	cgc	cga	gtg	gtg	aaa	aat	atg	gat	cgc	cac	gga	1171	
Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn	Met	Asp	Arg	His	Gly		
			345					350					355				
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Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg	Ile	Lys	Gly	Leu	Met		
		360					365					370					
ccc	cgt	gaa	ccc	agc	cat	att	tcc	acc	atc	gat	gaa	cat	agt	ctg	aac	1267	
Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp	Glu	His	Ser	Leu	Asn		
	375					380					385						
act	gtt	gca	gga	tgt	gcg	cta	gaa	act	gtg	acc	gtc	gcg	cgc	ccc	gat	1315	
Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr	Val	Ala	Arg	Pro	Asp		
390					395					400					405		
ctt	tta	gtt	ttg	gga	gcc	ttg	tac	cac	gac	att	ggc	aag	ggc	ttc	ccg	1363	
Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile	Gly	Lys	Gly	Phe	Pro		
				410					415					420			
cgt	cca	cac	gaa	caa	gta	ggt	gca	gag	atg	gtg	gcg	agg	gct	gca	agc	1411	
Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val	Ala	Arg	Ala	Ala	Ser		
			425					430					435				
cgc	atg	gga	ttg	aac	ctt	cgc	gat	cgt	gcc	agc	gtg	caa	acg	ctg	gtc	1459	
Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser	Val	Gln	Thr	Leu	Val		
		440					445					450					
gcc	gag	cac	acc	gcg	gtg	gcc	aaa	atc	gcc	gcg	cgc	ctt	gat	ccc	tcc	1507	
Ala	Glu	His	Thr	Ala	Val	Ala	Lys	Ile	Ala	Ala	Arg	Leu	Asp	Pro	Ser		
	455					460					465						
tcg	gag	ggc	gcc	gtc	gat	aag	ctg	ctt	gat	gct	gtt	agg	tat	gac	ctg	1555	
Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala	Val	Arg	Tyr	Asp	Leu		
470					475					480					485		
gtg	aca	ttg	aat	ctg	ctt	gag	gtg	cta	aca	gaa	gct	gat	gcg	aaa	gcc	1603	
Val	Thr	Leu	Asn	Leu	Leu	Glu	Val	Leu	Thr	Glu	Ala	Asp	Ala	Lys	Ala		
				490					495					500			
acg	ggg	cct	ggc	gtg	tgg	acg	gcg	cgt	ttg	gag	cat	gcg	ctg	cgg	att	1651	
Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu	His	Ala	Leu	Arg	Ile		
			505					510					515				
gtg	tgc	aag	cgt	gcg	cgt	gat	cgc	ctc	acc	gat	att	cgc	ccg	gtt	gcg	1699	
Val	Cys	Lys	Arg	Ala	Arg	Asp	Arg	Leu	Thr	Asp	Ile	Arg	Pro	Val	Ala		
		520					525					530					
ccg	atg	att	gcg	cca	cgt	agt	gaa	att	ggt	ttg	gtg	gaa	cgc	gat	ggc	1747	
Pro	Met	Ile	Ala	Pro	Arg	Ser	Glu	Ile	Gly	Leu	Val	Glu	Arg	Asp	Gly		
	535					540					545						
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Val	Phe	Thr	Val	Gln	Trp	His	Gly	Glu	Asp	Leu	His	Arg	Ile	Leu	Gly		
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Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg Ala Asn Gly Pro Gln																				
585 590 595																				
gat ttt gat ccg cag cat ttc ctg cag gca tat caa tcc ggt gtg ttt	1939																			
Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr Gln Ser Gly Val Phe																				
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Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr Ala Thr Phe Trp His																				
615 620 625																				
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Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu Lys Pro Gly Phe Asp																				
665 670 675																				
cga gca acg gtg gaa cgc tcc gta gtc agg tcg ttg gca ggt agc	2176																			
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<211> 692

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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35 40 45

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Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val
65 70 75 80

Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala
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Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu

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Arg	Gly	Gly	Leu	Arg	Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly
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His	Leu	Cys	Asn	Leu	Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu
			180					185					190		
Asp	Ala	Arg	Thr	Leu	Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val
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Asp	Asp	Gly	Leu	Thr	Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro
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Arg	Arg	Thr	Gly	Phe	Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp
			260					265					270		
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Cys	Pro	Pro	Leu	Pro	Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe
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Phe	Arg	Ile	Leu	Ser	Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn
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Ile	Lys	Gly	Leu	Met	Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp
	370					375					380				
Glu	His	Ser	Leu	Asn	Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr
385					390					395					400
Val	Ala	Arg	Pro	Asp	Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile
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Gly	Lys	Gly	Phe	Pro	Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val
			420					425					430		
Ala	Arg	Ala	Ala	Ser	Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser
			435				440					445			

Val Gln Thr Leu Val Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala
 450 455 460
 Arg Leu Asp Pro Ser Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala
 465 470 475 480
 Val Arg Tyr Asp Leu Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu
 485 490 495
 Ala Asp Ala Lys Ala Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu
 500 505 510
 His Ala Leu Arg Ile Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp
 515 520 525
 Ile Arg Pro Val Ala Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu
 530 535 540
 Val Glu Arg Asp Gly Val Phe Thr Val Gln Trp His Gly Glu Asp Leu
 545 550 555 560
 His Arg Ile Leu Gly Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala
 565 570 575
 Ala Arg Met Leu Ala Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg
 580 585 590
 Ala Asn Gly Pro Gln Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr
 595 600 605
 Gln Ser Gly Val Phe Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr
 610 615 620
 Ala Thr Phe Trp His Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg
 625 630 635 640
 Thr Gly Ala Ile Phe Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp
 645 650 655
 Ile Asn Ala Val Thr Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu
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 Leu Ala Gly Ser
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Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile Leu Glu Gly Ala Arg
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Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala Thr Val Arg Arg Leu
                        25                30                35
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Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile Phe His His Phe Gly
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Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg Glu Asp Ala Ala Arg
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Met Ala Glu Val Val Ser Glu Asn Gly Leu Val Glu Val Met Arg Gly
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Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met Ser Val Arg Leu Glu
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Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe Arg Ala Lys Trp Ile
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Asp His Gln Ser Val Leu Asp Glu Ala Val Arg Val Arg Leu Ser Arg
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Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val Pro Ile Glu Val Leu
                        135                140                145
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His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe Ile Ser Arg Leu Ala
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acc ggc gca tcc aca gaa gga ctg tcc gaa gta ttg gat ctg gtc gag 643
Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val Leu Asp Leu Val Glu
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gga act gtc cgt aaa cgc gac taaacgaccc ctgattcaca ctt 687
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<213> Corynebacterium glutamicum

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 Thr Val Arg Arg Leu Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile
 35 40 45
 Phe His His Phe Gly Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg
 50 55 60
 Glu Asp Ala Ala Arg Met Ala Glu Val Val Ser Glu Asn Gly Leu Val
 65 70 75 80
 Glu Val Met Arg Gly Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met
 85 90 95
 Ser Val Arg Leu Glu Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe
 100 105 110
 Arg Ala Lys Trp Ile Asp His Gln Ser Val Leu Asp Glu Ala Val Arg
 115 120 125
 Val Arg Leu Ser Arg Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val
 130 135 140
 Pro Ile Glu Val Leu His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe
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 Met Asn Ala Glu Glu
 1 5
 atc gga atg gcg ctg ctc aac gga cgc aaa gag cta ggc ctt aga caa 163
 Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu Leu Gly Leu Arg Gln
 10 15 20
 gga gag ctc gca gac tta gct gga gtt tct gaa cga ttc atc cgc gat 211
 Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu Arg Phe Ile Arg Asp
 25 30 35

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85

atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
 90 95 100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca gag 451
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala Glu
 105 110 115

atg gct cga ctc ctt gaa atg ctc acc cca gag cag ctg gaa cgt acc 499
 Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu Gln Leu Glu Arg Thr
 120 125 130

gaa gac ctg gtg gat atc att act gag ctt gca gag gtg tac ggt agc 547
 Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala Glu Val Tyr Gly Ser
 135 140 145

tgg aaa gag acc gac agc ggt tct taacagtttt ctccatctca act 594
 Trp Lys Glu Thr Asp Ser Gly Ser
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<211> 157

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu
 35 40 45

Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
 50 55 60

Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
 65 70 75 80

Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
 85 90 95

Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
 100 105 110

Glu Arg Asn Ala Glu Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu

115	120	125
Gln Leu Glu Arg Thr Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala		
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145	150	155

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 Met Leu Ala Gly Met
 1 5
 cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
 10 15 20
 aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
 25 30 35
 tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50
 tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65
 gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85
 atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
 90 95 100
 cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca 448
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala
 105 110 115

<210> 82
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<400> 82

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 20 25 30
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 35 40 45
 Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
 50 55 60
 Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
 65 70 75 80
 Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
 85 90 95
 Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
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 Glu Arg Asn Ala
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<210> 83
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 Met Thr Thr Ser Asn
 1 5
 ccc acc gcc gag atc att ggc gga cca gaa cga ttc ctc gag gcc gaa 163
 Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg Phe Leu Glu Ala Glu
 10 15 20
 ttg tcc cag cag att caa ttc ctc act gcc cgc gca cga gcc aag gga 211
 Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg Ala Arg Ala Lys Gly
 25 30 35
 tcc gcc aaa gga aac gaa gcc tta gtc gac ctc gga ctt aaa gtt cgc 259
 Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu Gly Leu Lys Val Arg
 40 45 50
 caa tac tcc aca ctg tcc cta gcg gcc agc gga tta aaa cca acc caa 307
 Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly Leu Lys Pro Thr Gln
 55 60 65
 cga gaa ttg gga gca ttt ctc gac cta gac cca agt cag att gtt gcc 355
 Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro Ser Gln Ile Val Ala
 70 75 80 85

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Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val Ala Arg Glu Val Asp
          90          95          100

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Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala Thr Glu Lys Gly Leu
          105          110          115

gaa att cac gac gaa gcc acc aaa cgc ctc ctc atc gcc gag ggt gaa 499
Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu Ile Ala Glu Gly Glu
          120          125          130

tct cta aaa aac ctc acc tcc gac gag caa gaa caa cta agg gaa ctg 547
Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu Gln Leu Arg Glu Leu
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ctg ctc aaa atc gcc ttt taagtctctt aaccacgccg gcc 588
Leu Leu Lys Ile Ala Phe
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Ala Arg Ala Lys Gly Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu
          35          40          45

Gly Leu Lys Val Arg Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly
          50          55          60

Leu Lys Pro Thr Gln Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro
          65          70          75          80

Ser Gln Ile Val Ala Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val
          85          90          95

Ala Arg Glu Val Asp Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala
          100          105          110

Thr Glu Lys Gly Leu Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu
          115          120          125

Ile Ala Glu Gly Glu Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu
          130          135          140

Gln Leu Arg Glu Leu Leu Leu Lys Ile Ala Phe
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<222> (101)..(694)

<223> RXA02667

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gga	gat	acc	gtc	gtt	tac	ccg	cac	cac	gga	gct	gca	att	att	tca	gcc	163
Gly	Asp	Thr	Val	Val	Tyr	Pro	His	His	Gly	Ala	Ala	Ile	Ile	Ser	Ala	
			10						15					20		

ctg	gag	cag	cgt	gaa	atg	aat	ggt	gag	acg	gtg	gac	tac	ctg	gtt	ctc	211
Leu	Glu	Gln	Arg	Glu	Met	Asn	Gly	Glu	Thr	Val	Asp	Tyr	Leu	Val	Leu	
			25					30					35			

cag	atc	aat	cat	tcc	gat	ctc	gtc	gtt	cgc	gtt	cca	gca	aag	aac	gct	259
Gln	Ile	Asn	His	Ser	Asp	Leu	Val	Val	Arg	Val	Pro	Ala	Lys	Asn	Ala	
		40					45					50				

gaa	ctc	gtt	ggc	gtg	cgt	gac	gtt	gtc	ggc	gag	gag	ggc	ctg	cag	aag	307
Glu	Leu	Val	Gly	Val	Arg	Asp	Val	Val	Gly	Glu	Glu	Gly	Leu	Gln	Lys	
		55				60					65					

gtt	ttc	tct	gtt	ctt	cgt	gaa	att	gac	gtc	gaa	gaa	gcc	ggc	aac	tgg	355
Val	Phe	Ser	Val	Leu	Arg	Glu	Ile	Asp	Val	Glu	Glu	Ala	Gly	Asn	Trp	
70					75					80					85	

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Ser	Arg	Arg	Tyr	Lys	Ala	Asn	Gln	Glu	Arg	Leu	Ala	Ser	Gly	Asp	Val	
				90					95					100		

aac	aag	gtc	gct	gag	gtt	gtc	cgt	gac	ctg	tgg	cgt	cgt	gat	cag	gat	451
Asn	Lys	Val	Ala	Glu	Val	Val	Arg	Asp	Leu	Trp	Arg	Arg	Asp	Gln	Asp	
		105						110					115			

cgt	ggc	ctt	tcc	gct	ggt	gag	aag	cgc	atg	ctc	tcc	aag	gcg	cgt	cag	499
Arg	Gly	Leu	Ser	Ala	Gly	Glu	Lys	Arg	Met	Leu	Ser	Lys	Ala	Arg	Gln	
		120					125					130				

gtt	ctt	gtt	ggt	gag	ctc	gcg	ctc	gcc	gaa	acc	gtg	gac	gat	gag	aag	547
Val	Leu	Val	Gly	Glu	Leu	Ala	Leu	Ala	Glu	Thr	Val	Asp	Asp	Glu	Lys	
		135				140					145					

gcg	gat	gct	ttc	ctc	agc	cag	gtc	gat	gag	acc	att	gct	cgc	cac	cgc	595
Ala	Asp	Ala	Phe	Leu	Ser	Gln	Val	Asp	Glu	Thr	Ile	Ala	Arg	His	Arg	
150					155					160					165	

gct	gac	ctg	ctc	ggc	gac	gag	gaa	gag	aag	aag	gac	gca	ttc	gac	gac	643
Ala	Asp	Leu	Leu	Gly	Asp	Glu	Glu	Glu	Lys	Lys	Asp	Ala	Phe	Asp	Asp	
			170						175					180		

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Phe	Asp	Asp	Ser	Asp	Val	Asp	Leu	Asp	Asp	Leu	Ser	Phe	Asp	Asp	Glu	

185

190

195

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Asp

717

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<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Glu Phe Lys Val Gly Asp Thr Val Val Tyr Pro His His Gly Ala
1 5 10 15

Ala Ile Ile Ser Ala Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val
20 25 30

Asp Tyr Leu Val Leu Gln Ile Asn His Ser Asp Leu Val Val Arg Val
35 40 45

Pro Ala Lys Asn Ala Glu Leu Val Gly Val Arg Asp Val Val Gly Glu
50 55 60

Glu Gly Leu Gln Lys Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu
65 70 75 80

Glu Ala Gly Asn Trp Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu
85 90 95

Ala Ser Gly Asp Val Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp
100 105 110

Arg Arg Asp Gln Asp Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu
115 120 125

Ser Lys Ala Arg Gln Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr
130 135 140

Val Asp Asp Glu Lys Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr
145 150 155 160

Ile Ala Arg His Arg Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys
165 170 175

Asp Ala Phe Asp Asp Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu
180 185 190

Ser Phe Asp Asp Glu Asp
195

<210> 87

<211> 479

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(456)

<223> RXA00348

<400> 87

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acc cgc gag cgc ctc gaa aac gcc caa tac cag gta caa cgc gac cga      48
Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
  1           5           10          15

gtc agg ggt gcc atg gaa gtc ttt atc gaa gcg gga atc gat ccc ggc      96
Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
          20           25           30

acc gtg ccg atc atg gaa tgc tgg atc aac aac cgc caa cac aac ttc      144
Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
          35           40           45

gaa gtg gcc aaa gaa ctt cta gaa aca cac cca gac ctc acc gca gta      192
Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
          50           55           60

ctc tgt acc gtc gat gca ctg gca ttc ggc gtt ctg gaa tac ctt aaa      240
Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
          65           70           75           80

agc gta ggt aaa tca gcg cct gca gat cta tcc ctc act ggt ttc gat      288
Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
          85           90           95

ggc acc cac atg gca ctc gca cgg gat ctc acc acc gtc atc caa ccc      336
Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
          100          105          110

aac aaa ctc aaa ggg ttc aaa gcc ggc gaa aca ctg ttg aaa atg att      384
Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
          115          120          125

gac aaa gaa tac gtg gaa cca gaa gtg gaa ttg gaa act tcc ttc cac      432
Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
          130          135          140

cca ggt tcc acg gtt gcg cca atc taggcttgtagt gcacttttcg tgc      479
Pro Gly Ser Thr Val Ala Pro Ile
          145          150

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<210> 88

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
  1           5           10          15

Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
          20           25           30

Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
          35           40           45

Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
          50           55           60

```

Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
65 70 75 80

Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
85 90 95

Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
100 105 110

Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
115 120 125

Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
130 135 140

Pro Gly Ser Thr Val Ala Pro Ile
145 150

<210> 89

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01500

<400> 89

acaccctcac ctggaatttt gcagaaatag ggcaagaatc aaaatagtgg gaaatcccca 60

tgtttcgcga agtcccattg ttggagtttag gcttataccc atg gct acg cat cca 115
Met Ala Thr His Pro
1 5

gat att ccc aca gag ttg ctt gaa tct ccg agc tat caa ctt gaa cga 163
Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser Tyr Gln Leu Glu Arg
10 15 20

ctt cga cga cgc act cgt gac cat gtt gag gcc gaa ttg gcc aag cat 211
Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala Glu Leu Ala Lys His
25 30 35

gag acc acg atg agg gaa ttc tgg acg ctt aca tgt ctg gtt cat tcc 259
Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr Cys Leu Val His Ser
40 45 50

gac gct gca agc cag tca gtt ctg tgt gag ctg ctg gcc att gat gca 307
Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu Leu Ala Ile Asp Ala
55 60 65

tcg gat atg gtc aga ctc gtt gac tca ctt gag gta cgc ggc tgg gcg 355
Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu Val Arg Gly Trp Ala
70 75 80 85

aaa agg gaa cgt gat ccc aaa gac cgt cgt cgc caa att gtt gcg tca 403
Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg Gln Ile Val Ala Ser
90 95 100

```

acg aag aag gga aaa aac gcc cag gcg gat ctg cac aaa gtt gtg ctt 451
Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu His Lys Val Val Leu
      105                      110                      115

gag gca gag gat gct gcg ttg gat gag tct acg tcc aag cag ttg aag 499
Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr Ser Lys Gln Leu Lys
      120                      125                      130

cac ctt cgt aaa ttg gcc gca gca att atc tcc acc gaa gag gac 544
His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser Thr Glu Glu Asp
      135                      140                      145

taaataataac gtggcattga gca 567

```

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<210> 90
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

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<400> 90
Met Ala Thr His Pro Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser
  1              5              10              15

Tyr Gln Leu Glu Arg Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala
      20              25              30

Glu Leu Ala Lys His Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr
      35              40              45

Cys Leu Val His Ser Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu
      50              55              60

Leu Ala Ile Asp Ala Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu
      65              70              75              80

Val Arg Gly Trp Ala Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg
      85              90              95

Gln Ile Val Ala Ser Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu
      100              105              110

His Lys Val Val Leu Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr
      115              120              125

Ser Lys Gln Leu Lys His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser
      130              135              140

Thr Glu Glu Asp
145

```

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<210> 91
<211> 272
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (37)..(249)
<223> RXA01125

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<210> 92
<211> 71
<212> PRT
<213> Corynebacterium glutamicum
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<210> 93
<211> 804
<212> DNA
<213> Corynebacterium glutamicum
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<400> 93
cagttagggtg tcatccggat tttatctcaa accctaacac cccaggtggt gccactcatc 60

cggactcaaa	caagatgtgt	gcagatgaag	gagaaaagca	gtg	gaa	ggt	gta	cag	115
				Val	Glu	Gly	Val	Gln	
				1				5	
gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca	163								
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala									
	10	15	20						
gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga	211								
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly									
	25	30	35						
gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc	259								
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile									
	40	45	50						
acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa	307								
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu									
	55	60	65						
aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc	355								
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser									
	70	75	80	85					
atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa	403								
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu									
	90	95	100						
gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct	451								
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala									
	105	110	115						
gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt	499								
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg									
	120	125	130						
ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc	547								
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val									
	135	140	145						
cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc	595								
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly									
	150	155	160	165					
acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa	643								
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu									
	170	175	180						
gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct	691								
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala									
	185	190	195						
ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc	739								
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser									
	200	205	210						
gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga	781								
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg									
	215	220	225						

taatcaccaa agcgctaaaa agc

804

<210> 94

<211> 227

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

Val Glu Gly Val Gln Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly
1 5 10 15

Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val
20 25 30

Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp
35 40 45

Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
50 55 60

Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
65 70 75 80

Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
85 90 95

Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
100 105 110

Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
115 120 125

Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
130 135 140

Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
145 150 155 160

Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
165 170 175

Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
180 185 190

Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg
195 200 205

Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg
210 215 220

Arg Ala Arg
225

<210> 95

<211> 804

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(781)

<223> FRXA00822

<400> 95

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cagttaggtg tcattccggat tttatctcaa accctaacac cccaggtggt gccactcatc 60
cggactcaaa caagatgtgt gcagatgaag gagaaaagca gtg gaa ggt gta cag 115
Val Glu Gly Val Gln
1 5
gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
10 15 20
gtc aat aac ctg atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
25 30 35
gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
40 45 50
acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
55 60 65
aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctg tcc 355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
70 75 80 85
atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
90 95 100
gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
105 110 115
gac cac cca gct atc gct gag cag ctg ctg cgc gtt ctg gct cgt cgt 499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
120 125 130
ctg cgt cgc acc aac gct tcc ctg gct gac ctg atc ttc acc gac gtc 547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
135 140 145
cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc 595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly
150 155 160 165
acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctg act cag gaa 643
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu
170 175 180
gaa atc gca cag ctg gtc ggt gct tcc cgt gaa act gtg aat aag gct 691
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala
185 190 195
ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctg gag ggc aag tcc 739
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser

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200	205	210	
gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga			781
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg			
215	220	225	

taatcaccaa agcgctaaaa agc	804
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<210> 96
 <211> 227
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 96	
Val Glu Gly Val Gln Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly	
1 5 10 15	
Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val	
20 25 30	
Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp	
35 40 45	
Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala	
50 55 60	
Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met	
65 70 75 80	
Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala	
85 90 95	
Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu	
100 105 110	
Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg	
115 120 125	
Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu	
130 135 140	
Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu	
145 150 155 160	
Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His	
165 170 175	
Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu	
180 185 190	
Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg	
195 200 205	
Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg	
210 215 220	
Arg Ala Arg	
225	

<400> 98
Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
1 5 10 15
Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
20 25 30
Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
35 40 45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
 50 55 60
 Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
 65 70 75 80
 Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
 85 90 95
 Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
 100 105

<210> 99
 <211> 444
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(421)
 <223> FRXA00849

<400> 99
 gcaaagcttt cgctgctga ttgaccatat tgagtcgcag tgactcaagt ttccaggtaa 60
 actgggaaca aattttaggg aaagggagtt gaacctaacg atg gtt act tat aca 115
 Met Val Thr Tyr Thr
 1 5
 acc ctt cta gac aag ccg att tca gaa tct gcc cca cgg aaa gct cca 163
 Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala Pro Arg Lys Ala Pro
 10 15 20
 gag cca ctt ctc cgc gaa gct ctg ggt gca gct ctt cgt tct ttc cgt 211
 Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala Leu Arg Ser Phe Arg
 25 30 35
 gct gac aag ggc gtt act ttg cgt gag ctg gcg gaa gct tca cgt gtg 259
 Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala Glu Ala Ser Arg Val
 40 45 50
 tca cct ggt tat ctt tca gaa ttg gaa cgc ggc cgc aaa gag gtg tcc 307
 Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly Arg Lys Glu Val Ser
 55 60 65
 tct gag ctt ctt gcc tcc gtg tgc cac gct ttg ggg gcc agc gtt gcg 355
 Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu Gly Ala Ser Val Ala
 70 75 80 85
 gat gtg ttg atc gaa gct gca ggt tcc atg gcg ctg caa gca gcg cag 403
 Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala Leu Gln Ala Ala Gln
 90 95 100
 gaa gac ctc gct cgc gtc taagcgcattg ggtgggcgtc gaa 444
 Glu Asp Leu Ala Arg Val
 105

<210> 100
 <211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
 1              5              10              15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
          20              25              30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
          35              40              45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
 50              55              60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
 65              70              75              80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
          85              90              95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
          100              105

```

<210> 101

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXA02698

<400> 101

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catcctgttt tcaaagggtca agaagggtgct ttcattcccgc gcacgcgcag aaatacccta 60

aagattctcc attagagctc gaaccagcta aattaagact gtg agt tcc aac aat 115
                               Val Ser Ser Asn Asn
                               1              5

gaa tct tcc ttc gcc ctg ccc gac aat gaa cca ttg ctg acc ctt ccg 163
Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro Leu Leu Thr Leu Pro
          10              15              20

gag aca gcc gag cgc ctc ggc gtt gtt gtc acc aag gtg atg gat ctg 211
Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr Lys Val Met Asp Leu
          25              30              35

gtc aat gaa cac aaa ttg atc gtg gtc cgg cgc gac ggt att cgc tac 259
Val Asn Glu His Lys Leu Ile Val Val Arg Arg Asp Gly Ile Arg Tyr
          40              45              50

att cca gaa gct ttc ctg agc acc aag aag gaa aac acc aac cgt ttc 307
Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu Asn Thr Asn Arg Phe
          55              60              65

atc cct gga gtt att gcc ttg ctt gcc gac ggt ggc ttc agc gac gag 355
Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly Gly Phe Ser Asp Glu

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70              75              80              85
gaa atc ctc gcg ttc ctg ttt acc gaa gac gag acc ctt cct ggt cgc 403
Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu Thr Leu Pro Gly Arg
              90              95              100

ccc atc gat gca ctt cat ggc cag ttg gct cgt gaa gtt atg cga cgc 451
Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg Glu Val Met Arg Arg
              105              110              115

gct caa gca atg gcg ttc taagcgcttt ctaaaagatc taa 492
Ala Gln Ala Met Ala Phe
              120

```

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<210> 102
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

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<400> 102
Val Ser Ser Asn Asn Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro
  1              5              10              15

Leu Leu Thr Leu Pro Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr
              20              25              30

Lys Val Met Asp Leu Val Asn Glu His Lys Leu Ile Val Val Arg Arg
              35              40              45

Asp Gly Ile Arg Tyr Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu
  50              55              60

Asn Thr Asn Arg Phe Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly
  65              70              75              80

Gly Phe Ser Asp Glu Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu
              85              90              95

Thr Leu Pro Gly Arg Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg
              100              105              110

Glu Val Met Arg Arg Ala Gln Ala Met Ala Phe
              115              120

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<210> 103
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(427)
<223> RXA00350

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<400> 103
agattcggta ataaaaggta aaaatcaacc tgcttaggcg tctttcgctt aaatagcgta 60

gaatatcggg tcgatcgctt ttaaacactc aggaggatcc ttg ccg gcc aaa atc 115
              Leu Pro Ala Lys Ile

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	1	5	
acg gac act cgt ccc acc cca gaa tcc ctt cac gct gtt gaa gag gaa			163
Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His Ala Val Glu Glu Glu			
	10	15	20
acc gca gcc ggt gcc cgc agg att gtt gcc acc tat tct aag gac ttc			211
Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr Tyr Ser Lys Asp Phe			
	25	30	35
ttc gac ggc gtc act ttg atg tgc atg ctc ggc gtt gaa cct cag ggc			259
Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly Val Glu Pro Gln Gly			
	40	45	50
ctg cgt tac acc aag gtc gct tct gaa cac gag gaa gct cag cca aag			307
Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu Glu Ala Gln Pro Lys			
	55	60	65
aag gct aca aag cgg act cgt aag gca cca gct aag aag gct gct gct			355
Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala Lys Lys Ala Ala Ala			
	70	75	80
aag aaa acg acc aag aag acc act aag aaa act act aaa aag acc acc			403
Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr			
	90	95	100
gca aag aag acc aca aag aag tct taagccggat cttatatgga tga			450
Ala Lys Lys Thr Thr Lys Lys Ser			
	105		

<210> 104

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Leu Pro Ala Lys Ile Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His			
1	5	10	15
Ala Val Glu Glu Glu Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr			
	20	25	30
Tyr Ser Lys Asp Phe Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly			
	35	40	45
Val Glu Pro Gln Gly Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu			
	50	55	60
Glu Ala Gln Pro Lys Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala			
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Lys Lys Ala Ala Ala Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr			
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Thr Lys Lys Thr Thr Ala Lys Lys Thr Thr Lys Lys Ser			
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<213> Corynebacterium glutamicum

<220>

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<223> RXA02830

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Leu	Glu	Asp	Ser	Leu	Gly	Val	Ser	Leu	Phe	Glu	Arg	Ala	Gly	Arg	Gly	
1				5				10						15		

ctg	gcg	ctg	aca	ggg	gcg	ggc	gat	cag	ctt	ttg	tcg	cag	gcg	cgc	cgc	96
Leu	Ala	Leu	Thr	Gly	Ala	Gly	Asp	Gln	Leu	Leu	Ser	Gln	Ala	Arg	Arg	
			20					25					30			

ctg	atc	gcc	ctg	aac	gac	gag	gta	tac	gcc	cgc	ttg	aac	gcc	ggg	gcc	144
Leu	Ile	Ala	Leu	Asn	Asp	Glu	Val	Tyr	Ala	Arg	Leu	Asn	Ala	Gly	Ala	
		35					40					45				

tac	gag	ggc	gag	gtg	acg	ctg	ggc	gtg	cct	caa	gac	gtg	atc	tac	ccc	192
Tyr	Glu	Gly	Glu	Val	Thr	Leu	Gly	Val	Pro	Gln	Asp	Val	Ile	Tyr	Pro	
	50					55					60					

gtc	atc	ccg	cgc	gtc	ttg	cag	caa	ttc	gcc	cgc	gat	ttt	ccc	cgc	gtg	240
Val	Ile	Pro	Arg	Val	Leu	Gln	Gln	Phe	Ala	Arg	Asp	Phe	Pro	Arg	Val	
65					70					75					80	

caa	att	cac	ctg	atc	tcg	aac	ttc	acg	ctg	atg	ctg	aaa	gaa	cag	ttc	288
Gln	Ile	His	Leu	Ile	Ser	Asn	Phe	Thr	Leu	Met	Leu	Lys	Glu	Gln	Phe	
			85						90					95		

cgc	cgc	ggc	gaa	atc	gac	gtg	atg	ctg	acg	acc	gag	gac	gag	ctg	ggc	336
Arg	Arg	Gly	Glu	Ile	Asp	Val	Met	Leu	Thr	Thr	Glu	Asp	Glu	Leu	Gly	
			100					105					110			

gag	ggc	ggc	gag	acg	ctg	gcc	cag	cgc	gag	ctg	atc	tgg	gtc	ggc	gca	384
Glu	Gly	Gly	Glu	Thr	Leu	Ala	Gln	Arg	Glu	Leu	Ile	Trp	Val	Gly	Ala	
		115					120					125				

ccg	ggc	ggg	tcg	gcg	tgg	acc	cgc	agg	ccg	ctg	ccc	ttg	gcg	ttt	gaa	432
Pro	Gly	Gly	Ser	Ala	Trp	Thr	Arg	Arg	Pro	Leu	Pro	Leu	Ala	Phe	Glu	
	130					135					140					

cgc	gcc	tgc	att	ttc	cgg	tct	ttc	ttg	cag	cgc	cgc	ttg	gat	gcc	aac	480
Arg	Ala	Cys	Ile	Phe	Arg	Ser	Phe	Leu	Gln	Arg	Arg	Leu	Asp	Ala	Asn	
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agc	atc	tat	tgg	caa												495
Ser	Ile	Tyr	Trp	Gln												
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<210> 106

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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1	5	10	15
Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg	20	25	30
Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala	35	40	45
Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro	50	55	60
Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val	65	70	75
Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe	85	90	95
Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly	100	105	110
Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala	115	120	125
Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu	130	135	140
Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn	145	150	155
Ser Ile Tyr Trp Gln	165		

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 Met Ala Arg Lys Leu
 1 5
 gaa cat cca tct ttg gcc gag atg aat tta aat gcc atc atg ttt gcg 163
 Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn Ala Ile Met Phe Ala
 10 15 20
 ctg tcg gat cct att agg cga caa atc ctg tcg cag ctg tcg tgc gga 211
 Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser Gln Leu Ser Cys Gly
 25 30 35
 cat aat gat cag gca tgt gtt gcc ttc gag ctt cca gta tct aaa tcc 259
 His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu Pro Val Ser Lys Ser
 40 45 50

acc tca acg cac cac ttc cgc gta ctc cgt gag gcg ggt ctg att act 307
 Thr Ser Thr His His Phe Arg Val Leu Arg Glu Ala Gly Leu Ile Thr
 55 60 65

cag cgc tat gaa gga act gcc att cta agt gcg ctg cgc agc gaa gat 355
 Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala Leu Arg Ser Glu Asp
 70 75 80 85

atg gaa gcg cgt ttt ccg gga ctg ctg act tct gtc atg cga gcg gaa 403
 Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser Val Met Arg Ala Glu
 90 95 100

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 Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
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atc 459

<210> 108
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 <213> Corynebacterium glutamicum

<400> 108
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Gln Leu Ser Cys Gly His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu
 35 40 45

Pro Val Ser Lys Ser Thr Ser Thr His His Phe Arg Val Leu Arg Glu
 50 55 60

Ala Gly Leu Ile Thr Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala
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Leu Arg Ser Glu Asp Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser
 85 90 95

Val Met Arg Ala Glu Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
 100 105 110

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 <212> DNA
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Met Gly Gln Gln Glu
1 5

att atc gag gac tcc acc gag agc ggt att aag gtt tta gac cgc act 163
Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys Val Leu Asp Arg Thr
10 15 20

gta tta atc ctc aat gtc atc gca gaa cag cct cga tcg ttg gca gag 211
Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro Arg Ser Leu Ala Glu
25 30 35

ctc gca gct gcc acc gat ctg ccc agg gct aca gcc cac cgc ctc gcc 259
Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr Ala His Arg Leu Ala
40 45 50

tca gcg ctt gag gta cac ggc atg ttg gca cgc tcc cgc gat aat aga 307
Ser Ala Leu Glu Val His Gly Met Leu Ala Arg Ser Arg Asp Asn Arg
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tgg acc atc ggc gca cgg ctt gcc tca ttg ggt gca cgc ggc gct gac 355
Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly Ala Arg Gly Ala Asp
70 75 80 85

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Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala Asp Leu Met Glu Arg
90 95 100

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Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr Gly Thr Thr Arg Thr
105 110 115

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Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu Lys Asn Val Val Pro
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Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser Ala Ala Arg Val Phe
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Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val Phe Ser Arg Glu Glu
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Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu Ser Val Gly Glu Arg
170 175 180

gag ctc ggc ctt gct agc ctc tcc tcc cct gtt ttt gat tcc aac gga 691
Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val Phe Asp Ser Asn Gly
185 190 195

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Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val Ala Glu Arg Leu Lys
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ccc cac ccc gcc gcc atg tgg ggc acc gag ctt atc gac gcc gcc gag 787
Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu Ile Asp Ala Ala Glu

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 35 40 45
 Ala His Arg Leu Ala Ser Ala Leu Glu Val His Gly Met Leu Ala Arg
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 Ser Arg Asp Asn Arg Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly
 65 70 75 80
 Ala Arg Gly Ala Asp Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala
 85 90 95
 Asp Leu Met Glu Arg Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr
 100 105 110
 Gly Thr Thr Arg Thr Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu
 115 120 125
 Lys Asn Val Val Pro Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser
 130 135 140
 Ala Ala Arg Val Phe Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val
 145 150 155 160
 Phe Ser Arg Glu Glu Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu
 165 170 175
 Ser Val Gly Glu Arg Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val
 180 185 190
 Phe Asp Ser Asn Gly Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val
 195 200 205
 Ala Glu Arg Leu Lys Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu
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 Met Asp Gln Thr Leu
 1 5

aaa gtt tta gta att gat gat gat ttc cgc gtc gcc ggc att cac gcc 163
 Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val Ala Gly Ile His Ala
 10 15 20

tcc atc gtt gat gcg tcc cct gga ttt tgc gtg gtc ggt acc gcg cgt 211
 Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val Val Gly Thr Ala Arg
 25 30 35

acc ctc gca gag gca aaa acc ctg atc gcc aca ttt tcc ccg gat ctc 259
 Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr Phe Ser Pro Asp Leu
 40 45 50

cta ctt gtt gat gtc tac ctc ccc gac ggc gat ggc att gac ctc gtg 307
 Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp Gly Ile Asp Leu Val
 55 60 65

ggc acc tcc aat att gat gcg ttt gtg ctc agc gca gcc gat gac atc 355
 Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser Ala Ala Asp Asp Ile
 70 75 80 85

aaa aca gtt cga cgc gcc atg cgt gcc ggg gca ctc gga tat ctg ctc 403
 Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala Leu Gly Tyr Leu Leu
 90 95 100

aaa cca ttt ccc caa aaa cgt ctc gtg gaa cgc ctt gac cgt tac gtc 451
 Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg Leu Asp Arg Tyr Val
 105 110 115

cgc tac cgc cat gtc tta tcc ggc acc caa gga ctt tcc caa gac aaa 499
 Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly Leu Ser Gln Asp Lys
 120 125 130

att gac cag gca acc gca atc ctc aac ggc acc caa gcg ccg gtc acc 547
 Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr Gln Ala Pro Val Thr
 135 140 145

gtc tct aga tcc gcc aca gag caa tta ctt ctc gac gcc ctg gaa ggc 595
 Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu Asp Ala Leu Glu Gly
 150 155 160 165

caa gaa ctc tcc gca aca gaa gct tcc gaa gct gcc gga gtt tca cgt 643
 Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala Ala Gly Val Ser Arg
 170 175 180

gcc aca gca cag cgc agg ctg gca gcg atg gct agc caa ggt gtg atc 691
 Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala Ser Gln Gly Val Ile

185 190 195
 cag gtt cgc ctt cgg tac gga cag tcc ggg cga cca gaa cat cta tat 739
 Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg Pro Glu His Leu Tyr
 200 205 210

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 Ser Lys Pro Leu Leu
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<210> 112
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 35 40 45
 Phe Ser Pro Asp Leu Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp
 50 55 60
 Gly Ile Asp Leu Val Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser
 65 70 75 80
 Ala Ala Asp Asp Ile Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala
 85 90 95
 Leu Gly Tyr Leu Leu Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg
 100 105 110
 Leu Asp Arg Tyr Val Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly
 115 120 125
 Leu Ser Gln Asp Lys Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr
 130 135 140
 Gln Ala Pro Val Thr Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu
 145 150 155 160
 Asp Ala Leu Glu Gly Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala
 165 170 175
 Ala Gly Val Ser Arg Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala
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 210 215

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 <223> RXA00182

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 Met Thr Ser His Leu
 1 5
 ctt cac ggt ctc tgg atc aaa gat cgc ggt ctg caa ctg tgg att gag 163
 Leu His Gly Leu Trp Ile Lys Asp Arg Gly Leu Gln Leu Trp Ile Glu
 10 15 20
 cag gtc gaa ggg cac cga att gtg ctt cca gag gcg gtg gaa aaa ggc 211
 Gln Val Glu Gly His Arg Ile Val Leu Pro Glu Ala Val Glu Lys Gly
 25 30 35
 acg ttc ccg ccg gta gtg gag caa atc ctc gac ggg aaa acc ttc cgc 259
 Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp Gly Lys Thr Phe Arg
 40 45 50
 gcg cgc atg aat gtg cat ctg cgc act ccg aaa ggg cgc cat gtt gag 307
 Ala Arg Met Asn Val His Leu Arg Thr Pro Lys Gly Arg His Val Glu
 55 60 65
 ctg ccc acg cca aca gca gct ttt acc cct gaa gaa gca gtc acg gtt 355
 Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu Glu Ala Val Thr Val
 70 75 80 85
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 Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr Pro Ala Ala Thr Arg
 90 95 100
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 Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp Trp Leu Ile Val Met
 105 110 115
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 Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly Arg Val Thr Leu Arg
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 135 140 145
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 Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met Asn His Ala Ala Pro
 150 155 160 165
 ggt att ttg cgg att aat ggt ggc cga gat ttg gcc gga agc atg tcc 643
 Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu Ala Gly Ser Met Ser
 170 175 180
 aat gag ctt ccg cac tgg atc gcc aac gcc att ttg cgt gat tac cgc 691

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Asp	Glu	Thr	Met	Pro	Tyr	Ala	Arg	His	Glu	Phe	Val	Glu	Ala	Leu	Leu		
		200					205					210					
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Phe	Asn	His	Ser	Leu	Arg	Lys	Gly	Ser	Thr	Met	Leu	Thr	His	Ala	Leu		
	215					220					225						
aat	cag	tgg	aaa	aac	acc	att	aca	tct	gcg	tct	ttg	cag	ctg	gtg	att		835
Asn	Gln	Trp	Lys	Asn	Thr	Ile	Thr	Ser	Ala	Ser	Leu	Gln	Leu	Val	Ile		
230					235					240					245		
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Leu	Val	Glu	Glu	Pro	Pro	Ala	Glu	Ser	Asp	Tyr	Glu	Asp	Pro	Met	Asp		
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Ser	Val	Trp	Pro	Val	Arg	Leu	Met	Val	Arg	Thr	Gly	Val	Asp	Ala	Pro		
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Gln	Ala	Ile	Gln	Lys	Gly	Ser	Ile	Asp	Ser	Gly	Gly	Met	Glu	Gln	Leu		
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Ala	Arg	Glu	Asp	Ala	Met	Leu	Gly	His	Met	Val	Asp	Ile	Ala	Gln	Asn		
310					315					320					325		
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Gly	Asp	Trp	Asp	Ile	Phe	Leu	Thr	Thr	Glu	Glu	Ile	Val	Asn	Phe	Ile		
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Ser	His	Asp	Val	Ala	Lys	Leu	Arg	Lys	Ala	Gly	Ile	Pro	Val	Met	Leu		
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Pro	Lys	Ala	Trp	Ser	Thr	Tyr	Glu	Thr	Arg	Ala	Gln	Val	Glu	Ala	Arg		
		360					365					370					
acg	ccg	aat	gat	gcc	gcg	gac	tct	tca	acc	aag	gca	atc	att	ggt	ctt		1267
Thr	Pro	Asn	Asp	Ala	Ala	Asp	Ser	Ser	Thr	Lys	Ala	Ile	Ile	Gly	Leu		
		375				380					385						
gac	cag	ctc	gtg	gaa	tac	aac	tgg	cgc	atc	agc	gtc	ggc	gat	att	cag		1315
Asp	Gln	Leu	Val	Glu	Tyr	Asn	Trp	Arg	Ile	Ser	Val	Gly	Asp	Ile	Gln		
390					395					400					405		
ctg	tcc	gac	gaa	gag	atg	cgc	gaa	ctc	atc	gat	tcc	aaa	aca	ggc	ctc		1363
Leu	Ser	Asp	Glu	Glu	Met	Arg	Glu	Leu	Ile	Asp	Ser	Lys	Thr	Gly	Leu		
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Ile	Arg	Leu	Arg	Gly	Asp	Trp	Val	Met	Ala	Asp	Gln	Asp	Ala	Leu	Arg		

425						430						435						
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Arg	Ile	Thr	Ser	Tyr	Met	Glu	Glu	Leu	Ser	Lys	Ser	Ser	Glu	Lys	Arg			
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gcg	cgc	acc	gaa	atg	gaa	aaa	gtg	gcc	atg	cag	gcc	aaa	ctc	gcc	gaa	1507		
Ala	Arg	Thr	Glu	Met	Glu	Lys	Val	Ala	Met	Gln	Ala	Lys	Leu	Ala	Glu			
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Ala	Asn	Gly	Glu	Glu	Gly	Trp	Gln	Leu	Leu	Ala	Ala	Lys	Ala	Glu	Thr			
470					475					480					485			
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Leu	Arg	Lys	Glu	Phe	Asn	Glu	Lys	Phe	Ser	Gly	Asp	Gly	Gln	Gly	Glu			
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gta	acc	ctt	gct	gaa	ctg	cgc	gaa	atc	gca	ctg	aaa	gcc	gcc	gaa	aac	1651		
Val	Thr	Leu	Ala	Glu	Leu	Arg	Glu	Ile	Ala	Leu	Lys	Ala	Ala	Glu	Asn			
			505					510					515					
gaa	cca	gtg	gaa	ttc	acc	ggc	tgc	caa	tgg	ttc	aac	tcc	ttg	ctc	ggc	1699		
Glu	Pro	Val	Glu	Phe	Thr	Gly	Ser	Gln	Trp	Phe	Asn	Ser	Leu	Leu	Gly			
		520					525					530						
ggc	acc	gaa	aca	ccc	gcg	ccg	gtg	cgc	gtc	gac	atc	ccc	gac	acg	gtc	1747		
Gly	Thr	Glu	Thr	Pro	Ala	Pro	Val	Arg	Val	Asp	Ile	Pro	Asp	Thr	Val			
	535					540					545							
ctt	gct	gac	ctg	cgc	gaa	tac	cag	cga	cgc	ggc	gtg	gac	tgg	ctg	tac	1795		
Leu	Ala	Asp	Leu	Arg	Glu	Tyr	Gln	Arg	Arg	Gly	Val	Asp	Trp	Leu	Tyr			
550					555					560					565			
tgg	atg	tcc	gca	aat	aat	tta	ggt	gca	gtg	ctt	gcc	gac	gac	atg	ggc	1843		
Trp	Met	Ser	Ala	Asn	Asn	Leu	Gly	Ala	Val	Leu	Ala	Asp	Asp	Met	Gly			
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Leu	Gly	Lys	Thr	Leu	Gln	Leu	Leu	Ser	Leu	Leu	Ala	Val	Glu	Arg	Ala			
			585					590					595					
gaa	aac	cca	gag	ttg	gaa	cgc	ggc	ccg	acg	ctc	gtg	gtg	tgc	cca	aca	1939		
Glu	Asn	Pro	Glu	Leu	Glu	Arg	Gly	Pro	Thr	Leu	Val	Val	Cys	Pro	Thr			
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tct	gtg	gtg	gga	aac	tgg	gca	gcc	gag	gcg	gct	aaa	ttt	gtg	cct	tca	1987		
Ser	Val	Val	Gly	Asn	Trp	Ala	Ala	Glu	Ala	Ala	Lys	Phe	Val	Pro	Ser			
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cta	aag	gta	ttg	atg	cat	cac	ggc	ccg	cag	cgt	ttg	aat	gat	gcc	gat	2035		
Leu	Lys	Val	Leu	Met	His	His	Gly	Pro	Gln	Arg	Leu	Asn	Asp	Ala	Asp			
630					635					640					645			
ttc	ctg	agt	caa	tcc	aag	ggc	atg	gac	ttg	att	atc	acc	tca	tac	ggc	2083		
Phe	Leu	Ser	Gln	Ser	Lys	Gly	Met	Asp	Leu	Ile	Ile	Thr	Ser	Tyr	Gly			
				650					655					660				
gtg	atc	acc	cgc	gat	ttc	aaa	ctc	atg	ggc	cag	gta	ggc	ttt	gaa	cgc	2131		
Val	Ile	Thr	Arg	Asp	Phe	Lys	Leu	Met	Gly	Gln	Val	Gly	Phe	Glu	Arg			
			665					670					675					

gtc	gtg	ctc	gat	gaa	gcg	cag	gca	att	aaa	aac	tct	tcc	aca	cgc	gta	2179
Val	Val	Leu	Asp	Glu	Ala	Gln	Ala	Ile	Lys	Asn	Ser	Ser	Thr	Arg	Val	
		680					685					690				
tca	aag	gca	gtg	cgc	tcg	ttg	cct	tcc	cgc	cac	cgc	gtt	gca	ctg	act	2227
Ser	Lys	Ala	Val	Arg	Ser	Leu	Pro	Ser	Arg	His	Arg	Val	Ala	Leu	Thr	
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ggc	acg	ccc	gtg	gaa	aac	cgc	ctg	tct	gaa	atg	cgc	tcc	atc	ttg	gac	2275
Gly	Thr	Pro	Val	Glu	Asn	Arg	Leu	Ser	Glu	Met	Arg	Ser	Ile	Leu	Asp	
710					715					720					725	
ttc	tgc	aac	ccc	ggc	gtg	ctg	ggt	tct	gca	tcg	ttt	ttc	cgc	aac	cac	2323
Phe	Cys	Asn	Pro	Gly	Val	Leu	Gly	Ser	Ala	Ser	Phe	Phe	Arg	Asn	His	
				730					735					740		
ttt	gcc	aag	gcc	att	gag	cgt	gaa	caa	gac	gac	acc	atg	act	gag	cgc	2371
Phe	Ala	Lys	Ala	Ile	Glu	Arg	Glu	Gln	Asp	Asp	Thr	Met	Thr	Glu	Arg	
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ctc	cgc	cag	ctc	acc	gca	ccg	ttt	att	ttg	cga	cgc	ctc	aaa	acc	gac	2419
Leu	Arg	Gln	Leu	Thr	Ala	Pro	Phe	Ile	Leu	Arg	Arg	Leu	Lys	Thr	Asp	
		760					765					770				
ccg	aat	atc	atc	gac	gat	ctg	cct	gag	aaa	acc	gaa	cag	atc	atc	cgc	2467
Pro	Asn	Ile	Ile	Asp	Asp	Leu	Pro	Glu	Lys	Thr	Glu	Gln	Ile	Ile	Arg	
	775					780					785					
gtg	gat	atg	acc	acc	gaa	cag	gca	tct	ctg	tac	aaa	gcg	ctg	gtt	gaa	2515
Val	Asp	Met	Thr	Thr	Glu	Gln	Ala	Ser	Leu	Tyr	Lys	Ala	Leu	Val	Glu	
790					795					800					805	
gat	gtg	cag	aaa	caa	ctc	gat	gaa	cgc	caa	gga	atg	tca	cgt	aaa	ggc	2563
Asp	Val	Gln	Lys	Gln	Leu	Asp	Glu	Arg	Gln	Gly	Met	Ser	Arg	Lys	Gly	
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ctg	gtc	ctg	gcg	acc	atc	acg	cgc	atc	aag	cag	atc	tgt	aac	cac	cca	2611
Leu	Val	Leu	Ala	Thr	Ile	Thr	Arg	Ile	Lys	Gln	Ile	Cys	Asn	His	Pro	
			825					830					835			
gcg	cac	ttc	ctt	ggc	gac	ggc	tca	gag	gtg	aca	ctg	aaa	ggt	aaa	cac	2659
Ala	His	Phe	Leu	Gly	Asp	Gly	Ser	Glu	Val	Thr	Leu	Lys	Gly	Lys	His	
		840					845					850				
cgt	tcc	ggc	aag	gtg	gaa	gcg	ctc	atg	gaa	ctg	atc	gat	acg	gca	gta	2707
Arg	Ser	Gly	Lys	Val	Glu	Ala	Leu	Met	Glu	Leu	Ile	Asp	Thr	Ala	Val	
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aaa	gaa	gag	cgc	cgc	atg	ctg	atc	ttc	acc	cag	tac	gca	gcc	ttt	ggc	2755
Lys	Glu	Glu	Arg	Arg	Met	Leu	Ile	Phe	Thr	Gln	Tyr	Ala	Ala	Phe	Gly	
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cgt	att	ttg	gcg	ccg	tac	ctg	tct	gat	cga	ttg	ggc	acg	aat	atc	cca	2803
Arg	Ile	Leu	Ala	Pro	Tyr	Leu	Ser	Asp	Arg	Leu	Gly	Thr	Asn	Ile	Pro	
				890					895					900		
ttc	ctg	cac	ggc	ggc	gtg	acc	aaa	cca	gga	cgc	gac	cgc	atg	gtg	gcg	2851
Phe	Leu	His	Gly	Gly	Val	Thr	Lys	Pro	Gly	Arg	Asp	Arg	Met	Val	Ala	
			905					910					915			

gaa ttc caa tcc gaa gac gga cca ccg gca atg atc ctg tct ttg aaa 2899
 Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met Ile Leu Ser Leu Lys
 920 925 930

gcc ggc ggt act ggc ttg aac ctg aca gct gca tcc atc gtg gtc cac 2947
 Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala Ser Ile Val Val His
 935 940 945

atg gat aga tgg tgg aac cca gcc gtg gaa aac caa gca act gac cgt 2995
 Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn Gln Ala Thr Asp Arg
 950 955 960 965

gcc ttc cgc atc ggc cag cgc aaa aac gtg gat gta tac aag atg atc 3043
 Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp Val Tyr Lys Met Ile
 970 975 980

aca gtc gga acc atg gag gaa tcc atc caa gat atc ctc gat gga aaa 3091
 Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp Ile Leu Asp Gly Lys
 985 990 995

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 Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly Glu Gly Trp Ile Thr
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<213> Corynebacterium glutamicum

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Ala Val Glu Lys Gly Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp
 35 40 45

Gly Lys Thr Phe Arg Ala Arg Met Asn Val His Leu Arg Thr Pro Lys
 50 55 60

Gly Arg His Val Glu Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu
 65 70 75 80

Glu Ala Val Thr Val Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr
 85 90 95

Pro Ala Ala Thr Arg Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp
 100 105 110

Trp Leu Ile Val Met Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly

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Arg	Val	Thr	Leu	Arg	Thr	Val	Met	Met	Asp	Asn	Ala	Trp	Trp	Pro	Gln
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Trp	Gln	Leu	Ser	Ala	Ser	Leu	Ser	Glu	Arg	Gly	Trp	Leu	Ala	Glu	Met
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Asn	His	Ala	Ala	Pro	Gly	Ile	Leu	Arg	Ile	Asn	Gly	Gly	Arg	Asp	Leu
165				170				175							
Ala	Gly	Ser	Met	Ser	Asn	Glu	Leu	Pro	His	Trp	Ile	Ala	Asn	Ala	Ile
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Leu	Arg	Asp	Tyr	Arg	Asp	Glu	Thr	Met	Pro	Tyr	Ala	Arg	His	Glu	Phe
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Val	Glu	Ala	Leu	Leu	Phe	Asn	His	Ser	Leu	Arg	Lys	Gly	Ser	Thr	Met
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245				250				255							
Glu	Asp	Pro	Met	Asp	Ser	Val	Trp	Pro	Val	Arg	Leu	Met	Val	Arg	Thr
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Gly	Val	Asp	Ala	Pro	Gln	Ala	Ile	Gln	Lys	Gly	Ser	Ile	Asp	Ser	Gly
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Gly	Met	Glu	Gln	Leu	Arg	Ser	Gln	Tyr	Glu	Thr	Ala	Lys	Thr	Thr	Ser
290				295				300							
Met	Leu	Leu	Asp	Pro	Ala	Arg	Glu	Asp	Ala	Met	Leu	Gly	His	Met	Val
305				310				315				320			
Asp	Ile	Ala	Gln	Asn	Gly	Asp	Trp	Asp	Ile	Phe	Leu	Thr	Thr	Glu	Glu
325				330				335							
Ile	Val	Asn	Phe	Ile	Ser	His	Asp	Val	Ala	Lys	Leu	Arg	Lys	Ala	Gly
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Ile	Pro	Val	Met	Leu	Pro	Lys	Ala	Trp	Ser	Thr	Tyr	Glu	Thr	Arg	Ala
355				360				365							
Gln	Val	Glu	Ala	Arg	Thr	Pro	Asn	Asp	Ala	Ala	Asp	Ser	Ser	Thr	Lys
370				375				380							
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385				390				395				400			
Val	Gly	Asp	Ile	Gln	Leu	Ser	Asp	Glu	Glu	Met	Arg	Glu	Leu	Ile	Asp
405				410				415							
Ser	Lys	Thr	Gly	Leu	Ile	Arg	Leu	Arg	Gly	Asp	Trp	Val	Met	Ala	Asp
420				425				430							
Gln	Asp	Ala	Leu	Arg	Arg	Ile	Thr	Ser	Tyr	Met	Glu	Glu	Leu	Ser	Lys
435				440				445							

Ser Ser Glu Lys Arg Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln
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 Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala
 465 470 475 480
 Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly
 485 490 495
 Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu
 500 505 510
 Lys Ala Ala Glu Asn Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe
 515 520 525
 Asn Ser Leu Leu Gly Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp
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 Ile Pro Asp Thr Val Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly
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 Val Asp Trp Leu Tyr Trp Met Ser Ala Asn Asn Leu Gly Ala Val Leu
 565 570 575
 Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Leu Leu Ser Leu Leu
 580 585 590
 Ala Val Glu Arg Ala Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu
 595 600 605
 Val Val Cys Pro Thr Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala
 610 615 620
 Lys Phe Val Pro Ser Leu Lys Val Leu Met His His Gly Pro Gln Arg
 625 630 635 640
 Leu Asn Asp Ala Asp Phe Leu Ser Gln Ser Lys Gly Met Asp Leu Ile
 645 650 655
 Ile Thr Ser Tyr Gly Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln
 660 665 670
 Val Gly Phe Glu Arg Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn
 675 680 685
 Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His
 690 695 700
 Arg Val Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met
 705 710 715 720
 Arg Ser Ile Leu Asp Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser
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 Phe Phe Arg Asn His Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp
 740 745 750
 Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg
 755 760 765

Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr
 770 775 780
 Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr
 785 790 795 800
 Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly
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 Met Ser Arg Lys Gly Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln
 820 825 830
 Ile Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr
 835 840 845
 Leu Lys Gly Lys His Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu
 850 855 860
 Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln
 865 870 875 880
 Tyr Ala Ala Phe Gly Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu
 885 890 895
 Gly Thr Asn Ile Pro Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg
 900 905 910
 Asp Arg Met Val Ala Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met
 915 920 925
 Ile Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala
 930 935 940
 Ser Ile Val Val His Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn
 945 950 955 960
 Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp
 965 970 975
 Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp
 980 985 990
 Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly
 995 1000 1005
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                                         Met Ser Asp Glu Asn
                                         1           5

att aac gag ttt gag cag gac gag gat ctg aac ttc ggc gcg agc ttt 163
Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe
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agt gat gaa ttc gca gat gac gat ttc gat gca gaa gca gac gta gaa 211
Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu
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gca gat gct gct gca gag gcc tct gcc ctg gaa gct gag cag gat ctg 259
Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu Ala Glu Gln Asp Leu
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Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro
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gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac 355
Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp
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agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac 403
Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp
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gcg gat gca gag tac aag gct cgt ctg cgt aag ttc act cgt gag ctg 451
Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu
                        105                        110                        115

aag aag cag cct ggt gtt tgg tac atc att cag tgc tac tcc ggc tac 499
Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr
                        120                        125                        130

gag aac aag gtg aag gcg aac ctt gac atg cgt gct cag acc ctt gag 547
Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg Ala Gln Thr Leu Glu
                        135                        140                        145

gtt gag gat gac atc ttt gag gtt gtt gtt cct atc gag cag gtc act 595
Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr
                        150                        155                        160                        165

gag atc cgt gat ggt aag cgc aag ctg gtt aag cgt aag ttg ctg ccg 643
Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro
                        170                        175                        180

ggc tac gtt ttg gtc cgc atg gac atg aat gac cgc gtg tgg tct gtt 691
Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val
                        185                        190                        195

gtt cgc gat aca cct ggt gtg acc agc ttt gtg ggt aac gag ggc aat 739
Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn
                        200                        205                        210

gca act cct gtg aag cac cgc gat gtt gcg aag ttc ttg atg cct cag 787

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Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln
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gag cag gct gtt gtc acc ggt gag gct gct gct gcg gct gcc gag ggt 835
 Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala Ala Glu Gly
 230 235 240 245

gag cag gtt gtg gct atg cct acc gat acc aag aag cct cag gtt gct 883
 Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala
 250 255 260

gtg gac ttc act gtt ggt gag gct gtg acc att ctg act ggt gct ttc 931
 Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe
 265 270 275

gct tct gtt tct gca acg att tct tct atc gat cct gag ctg cag aag 979
 Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp Pro Glu Leu Gln Lys
 280 285 290

ctg gaa gtt ttg gtg tcc atc ttt ggt cgt gaa act cct gtt gat ctc 1027
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<213> Corynebacterium glutamicum

<400> 116

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 35 40 45

Ala Glu Gln Asp Leu Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala
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Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu
 65 70 75 80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp
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Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys
 100 105 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln
 115 120 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg
 130 135 140

Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Val Pro
 145 150 155 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys
 165 170 175

Arg Lys Leu Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp
 180 185 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val
 195 200 205

Gly Asn Glu Gly Asn Ala Thr Pro Val Lys His Arg Asp Val Ala Lys
 210 215 220

Phe Leu Met Pro Gln Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala
 225 230 235 240

Ala Ala Ala Glu Gly Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys
 245 250 255

Lys Pro Gln Val Ala Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile
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Leu Thr Gly Ala Phe Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp
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 Met Gln Pro Glu Glu
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gtg cac atc aag gac gag acc atc aag tta ggt cag ttc atc aaa ttg 163
 Val His Ile Lys Asp Glu Thr Ile Lys Leu Gly Gln Phe Ile Lys Leu
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gcc aac ctt gtc gaa tca ggc gga gcg gcc aaa gat gcc atc gct aac 211
 Ala Asn Leu Val Glu Ser Gly Gly Ala Ala Lys Asp Ala Ile Ala Asn
 25 30 35

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Gly Asp Val Thr Val Asn Gly Glu Val Asp Thr Arg Arg Gly Lys Thr
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 ctt cgc gat ggc gat gtg gtg tgc atc ggc gag gta tgc gcg cag gtg 307
 Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu Val Cys Ala Gln Val
 55 60 65
 tct act ggt gac gca gcc gac gac gat tat ttt gac gaa gcc acc gca 355
 Ser Thr Gly Asp Ala Ala Asp Asp Asp Tyr Phe Asp Glu Ala Thr Ala
 70 75 80 85
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 Arg Arg Gly Lys Thr Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu
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 Val Cys Ala Gln Val Ser Thr Gly Asp Ala Ala Asp Asp Asp Tyr Phe
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 Met

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 Met Ser Gln Lys Ile

	1	5	
ctc gtg gtt gat gat gat ccc gcc atc tcc gag atg ctc acc atc gtg			163
Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu Met Leu Thr Ile Val	10	20	
ctc agc gca gaa ggc ttt gac acc gta gct gtc acc gac ggc gca ctc			211
Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val Thr Asp Gly Ala Leu	25	30	35
gcc gtg gaa acc gcc tcc cgg gaa caa ccg gat ctg att ttg ctc gac			259
Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp Leu Ile Leu Leu Asp	40	45	50
ttg atg ctt cca ggc atg aac ggc atc gac att tgt cgc ctc atc cgc			307
Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile Cys Arg Leu Ile Arg	55	60	65
caa gaa tcc tcc gta ccc atc atc atg ctc acc gcc aaa acc gac acc			355
Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr Ala Lys Thr Asp Thr	70	75	80
gtt gat gtg gtg ctc ggt ttg gaa tcc ggt gca gac gat tac gtg aac			403
Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala Asp Asp Tyr Val Asn	90	95	100
aag cct ttc aaa gcg aaa gaa ctt gtc gcc cgc atc cgt gcc cgc ctc			451
Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg Ile Arg Ala Arg Leu	105	110	115
cgc gca acc gtg gac gag ccc agc gaa atc atc gaa gtc ggc gat ctg			499
Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile Glu Val Gly Asp Leu	120	125	130
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Ser Ile Asp Val Pro Ala His Thr Val Lys Arg Asn Gly Ala Glu Ile	135	140	145
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Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu Glu Leu Ala Arg Lys	150	155	160
cca cag caa gta ttc acc cgt gaa gaa ttg ctg ggc aaa gtg tgg ggc			643
Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu Gly Lys Val Trp Gly	170	175	180
tac cgc cac gca tcc gac act cga ctg gtc aac gtt cac gtt cag cgt			691
Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn Val His Val Gln Arg	185	190	195
ctg cgc gcc aag att gaa aaa gat cca gaa aat ccg cag atc gtc ctc			739
Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn Pro Gln Ile Val Leu	200	205	210
acc gtc cgc ggt gtt ggc tac aaa act ggc cac aac gat taagtttttc			788
Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His Asn Asp	215	220	225
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 <213> Corynebacterium glutamicum

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 35 40 45
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 Cys Arg Leu Ile Arg Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr
 65 70 75 80
 Ala Lys Thr Asp Thr Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala
 85 90 95
 Asp Asp Tyr Val Asn Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg
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 Ile Arg Ala Arg Leu Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile
 115 120 125
 Glu Val Gly Asp Leu Ser Ile Asp Val Pro Ala His Thr Val Lys Arg
 130 135 140
 Asn Gly Ala Glu Ile Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu
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 Glu Leu Ala Arg Lys Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu
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 Gly Lys Val Trp Gly Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn
 180 185 190
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 Asn Asp
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Met Val Ser Ala Thr
1 5

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Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile Val Ala Asp Tyr Ile
10 15 20

gcg tct cag gaa cct gtc gga tgc aag tca ctc ctc gag cgc cat aag 211
Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu Leu Glu Arg His Lys
25 30 35

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Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser Ser Gly Arg Val Pro
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Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser Ile His Asp Ile Lys
70 75 80 85

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Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu Gly Phe Leu Glu Gly
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Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser Val Gln Leu Leu Ser
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Gln Leu Thr His Gln Ala Ala Val Val Gln Leu Pro Thr Leu Lys Thr
120 125 130

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Ala Arg Val Lys His Cys Glu Val Val Pro Leu Ser Pro Met Arg Leu
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Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val Asp Gln Arg Asn Val
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Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val Asn Val Leu Arg Asp
170 175 180

ctg ctc aac ggc gcg cta ggg gag aaa acg ctg acg gct gca tca gat 691
Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu Thr Ala Ala Ser Asp
185 190 195

gcg ctg gaa gag ttg gct cag caa gcc cca acc gat att cgt gat gcc 739
Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr Asp Ile Arg Asp Ala
200 205 210

atg cgc cgc tgc tgc gat gtg ctg gtg aac acg ctt gtc gat caa ccc 787

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Ser	Asp	Arg	Leu	Ile	Leu	Ala	Gly	Thr	Ser	Asn	Leu	Thr	Arg	Leu	Ser		
230					235					240					245		
cgg	gaa	acc	tcc	gcg	agc	ctg	ccc	atg	gtt	tta	gaa	gcc	ttg	gaa	gag	883	
Arg	Glu	Thr	Ser	Ala	Ser	Leu	Pro	Met	Val	Leu	Glu	Ala	Leu	Glu	Glu		
				250					255					260			
cag	gtg	gtc	atg	ttg	aaa	ctg	ctg	tcc	aat	gtc	act	gat	ctt	gac	caa	931	
Gln	Val	Val	Met	Leu	Lys	Leu	Leu	Ser	Asn	Val	Thr	Asp	Leu	Asp	Gln		
			265					270					275				
gtg	cgc	gtg	cat	att	ggc	ggc	gaa	aat	gaa	gac	att	gag	ctg	cgc	agc	979	
Val	Arg	Val	His	Ile	Gly	Gly	Glu	Asn	Glu	Asp	Ile	Glu	Leu	Arg	Ser		
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gca	acg	gtg	att	acc	acc	ggt	tac	ggc	tcc	cag	ggc	agc	gca	ctg	ggc	1027	
Ala	Thr	Val	Ile	Thr	Thr	Gly	Tyr	Gly	Ser	Gln	Gly	Ser	Ala	Leu	Gly		
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Gly	Leu	Gly	Val	Val	Gly	Pro	Thr	Tyr	Met	Asp	Tyr	Ser	Gly	Thr	Ile		
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Ser	Lys	Val	Ser	Ala	Val	Ala	Lys	Tyr	Val	Gly	Arg	Val	Leu	Ala	Gly		
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Glu																	

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<212> PRT

<213> Corynebacterium glutamicum

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Leu	Glu	Arg	His	Lys	Leu	Asn	Val	Ser	Ser	Ala	Thr	Ile	Arg	Asn	Asp		
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Met	Ser	Val	Leu	Glu	Ser	Asp	Gly	Phe	Ile	Val	Gln	Glu	His	Ala	Ser		
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Ser	Gly	Arg	Val	Pro	Thr	Glu	Arg	Gly	Tyr	Arg	Leu	Phe	Val	Asp	Ser		
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Gly	Phe	Leu	Glu	Gly	Gly	Val	Asp	Leu	Glu	Asp	Val	Leu	Arg	Arg	Ser		

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Val	Gln	Leu	Leu	Ser	Gln	Leu	Thr	His	Gln	Ala	Ala	Val	Val	Gln	Leu
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Pro	Thr	Leu	Lys	Thr	Ala	Arg	Val	Lys	His	Cys	Glu	Val	Val	Pro	Leu
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			180					185					190		
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Leu	Val	Asp	Gln	Pro	Ser	Asp	Arg	Leu	Ile	Leu	Ala	Gly	Thr	Ser	Asn
225					230					235					240
Leu	Thr	Arg	Leu	Ser	Arg	Glu	Thr	Ser	Ala	Ser	Leu	Pro	Met	Val	Leu
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Thr	Asp	Leu	Asp	Gln	Val	Arg	Val	His	Ile	Gly	Gly	Glu	Asn	Glu	Asp
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Gly	Ser	Ala	Leu	Gly	Gly	Leu	Gly	Val	Val	Gly	Pro	Thr	Tyr	Met	Asp
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Tyr	Ser	Gly	Thr	Ile	Ser	Lys	Val	Ser	Ala	Val	Ala	Lys	Tyr	Val	Gly
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Met Leu Gly Asp Arg
1 5

acg cgc ctc cgc ctc ctc atc gcg ctg cat tat cac ggc ccc ggt gaa 163
Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr His Gly Pro Gly Glu
10 15 20

gcc acc gtc tca gaa ctc gcg gac atc gtc ggc gtc acc ctg ccc acg 211
Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly Val Thr Leu Pro Thr
25 30 35

gcc tcc gca gcg ctc caa ctg ctc gca gat aac gga gtg gtc gag tcc 259
Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn Gly Val Val Glu Ser
40 45 50

ttc aag gag ggg cgg gtg aca aga tat aag ctt gtc gac gcc acg acc 307
Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu Val Asp Ala Thr Thr
55 60 65

cac acc ttg ctt cac cac ctc ggg ggc acc cac cga cat taaaggggaac 356
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Val Thr Leu Pro Thr Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn
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Gly Val Val Glu Ser Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu
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Val Asp Ala Thr Thr His Thr Leu Leu His His Leu Gly Gly Thr His
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Arg His

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Met Thr Lys Arg Leu																5
1																
agc	ctt	gaa	ggg	ctc	cgc	tat	gcg	cag	gcc	gtc	gca	gaa	act	cac	tca	163
Ser	Leu	Glu	Gly	Leu	Arg	Tyr	Ala	Gln	Ala	Val	Ala	Glu	Thr	His	Ser	
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Phe	Ser	Ala	Ala	Ala	Arg	Glu	Tyr	Gly	Val	Thr	Gln	Pro	Ala	Leu	Ser	
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Asn	Gly	Ile	Ala	Lys	Leu	Glu	Asp	Arg	Leu	Gly	Glu	Gln	Leu	Phe	Asp	
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Arg	Ser	Thr	Gln	Gly	Val	Thr	Pro	Thr	Ser	Phe	Gly	Leu	His	Ile	Leu	
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Ser	Pro	Leu	Ile	Asn	Pro	Gln	Leu	Val	Ala	Arg	Thr	Tyr	Thr	Ala	Val	
105 110 115																
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Arg	Glu	Leu	Pro	Thr	Ala	His	Asp	Leu	Val	Leu	Arg	Glu	Ala	Asn	Met	
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Lys	Glu	Leu	His	Glu	Gly	Leu	Leu	Ala	Gly	Glu	Leu	Asn	Val	Ile	Leu	
135 140 145																
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Ile	Pro	Ala	Val	Lys	Pro	Leu	Pro	His	Phe	Glu	His	Arg	Ile	Ile	Asp	
150 155 160 165																
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Ser	Glu	Pro	Val	Val	Ile	Val	Glu	Ser	Thr	Gln	Asp	Ser	Thr	Asp	Pro	
170 175 180																
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Ile	Glu	Leu	Arg	Glu	Thr	Gln	His	Glu	Pro	Phe	Ile	Leu	Val	Pro	Asp	
185 190 195																
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Thr	Cys	Gly	Leu	Thr	Thr	Phe	Thr	Asn	Gln	Leu	Phe	Glu	Thr	Asn	Asp	
200 205 210																
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 Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala Met Leu Pro Leu Ser
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<211> 254

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<213> Corynebacterium glutamicum

<400> 126

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Gln Pro Ala Leu Ser Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly
 35 40 45

Glu Gln Leu Phe Asp Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe
 50 55 60

Gly Leu His Ile Leu Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp
 65 70 75 80

Ala Ile Thr Ala Glu Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser
 85 90 95

Ile Arg Val Gly Ile Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg
 100 105 110

Thr Tyr Thr Ala Val Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu
 115 120 125

Arg Glu Ala Asn Met Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu
 130 135 140

Leu Asn Val Ile Leu Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu
 145 150 155 160

His Arg Ile Ile Asp Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln
 165 170 175

Asp Ser Thr Asp Pro Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe
 180 185 190

Ile Leu Val Pro Asp Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu
 195 200 205

Phe Glu Thr Asn Asp Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala
 210 215 220

Ser Tyr Gln Val Leu Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala
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 Met Ser Asp Met Pro
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 aca aaa agg gtt gcc ccc gca cgc tca ctc acc gac caa gtc atg gat 163
 Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr Asp Gln Val Met Asp
 10 15 20
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 Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met Val Thr Gly Glu Trp
 25 30 35
 tac agc gtt tac cag gtc agc gac caa tta ggc att tcc cgc tcc ccc 259
 Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly Ile Ser Arg Ser Pro
 40 45 50
 gtc aga gac gcg ctg ctc cgc ctg gaa gaa gca ggg ctc atc cgc ttc 307
 Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala Gly Leu Ile Arg Phe
 55 60 65
 acc agg aac cgc gga ttc caa att gtc gaa acc aaa ccc tct gat gtc 355
 Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr Lys Pro Ser Asp Val
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 Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu Pro Ala Ala Ala Tyr
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 Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu His Glu Ala Asp Asp
 105 110 115
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 Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp Asn Asp Glu Glu Ala
 120 125 130
 ttt ttc acc cat gac cgg cag ttt cac cga caa att atg acc atg gga 547
 Phe Phe Thr His Asp Arg Gln Phe His Arg Gln Ile Met Thr Met Gly
 135 140 145
 cac tcc caa cgc ggg gct gac ctg gta gaa aaa cta cgc gca cac acc 595

His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys Leu Arg Ala His Thr
 150 155 160 165
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 Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys Arg Thr Leu Gly Asp
 170 175 180
 att ttg gaa gaa cac gaa cca atc ttg gat gcc atc aaa cga caa tca 691
 Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala Ile Lys Arg Gln Ser
 185 190 195
 gca gaa atg gca cga gcc acc atg cgg gag cat atc caa gtc acc gga 739
 Ala Glu Met Ala Arg Ala Thr Met Arg Glu His Ile Gln Val Thr Gly
 200 205 210
 aag cta cta cta gaa caa gca gtg gaa aaa tcc ggc gaa gga gct gct 787
 Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser Gly Glu Gly Ala Ala
 215 220 225
 cag aag att tgg gat cag tac acg gcg gga gtt taggcatatt tacctaataca 840
 Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
 230 235 240
 att 843
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 <213> Corynebacterium glutamicum
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 Met Ser Asp Met Pro Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr
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 Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met
 20 25 30
 Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly
 35 40 45
 Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala
 50 55 60
 Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr
 65 70 75 80
 Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu
 85 90 95
 Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu
 100 105 110
 His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp
 115 120 125
 Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln Phe His Arg Gln
 130 135 140
 Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys
 145 150 155 160

Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys
 165 170 175
 Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala
 180 185 190
 Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr Met Arg Glu His
 195 200 205
 Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser
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 Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
 225 230 235 240

<210> 129
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 gat aaa aca atg gtc acc gga gag tgg tac agc gtt tac cag gtc agc 96
 Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
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 gac caa tta ggc att tcc cgc tcc ccc gtc aga gac gcg ctg ctc cgc 144
 Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
 35 40 45
 ctg gaa gaa gca ggg ctc atc cgc ttc acc agg aac cgc gga ttc caa 192
 Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
 50 55 60
 att gtc gaa acc aaa ccc tct gat gtc gcc gaa att ttt gcc ctt cgt 240
 Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
 65 70 75 80
 cta ggc att gaa ccc gcc gca gca tac cgg gca gca cag cta cgc acc 288
 Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
 85 90 95
 gaa gaa cag ctc cac gaa gca gat gac atc att gca ctc atg gcg caa 336
 Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
 100 105 110
 gcc gag gcc gac aat gac gaa gaa gca ttt ttc acc cat gac cgg cag 384
 Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln

115	120	125	
ttt cac cga caa att atg acc atg gga cac tcc caa cgc ggg gct gac			432
Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp			
130	135	140	
ctg gta gaa aaa cta cgc gca cac acc cgt atc ctc ggt gct tct act			480
Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr			
145	150	155	160
gcc ggg aac aaa cgc acc ctt ggc gat att ttg gaa gaa cac gaa cca			528
Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro			
	165	170	175
atc ttg gat gcc atc aaa cga caa tca gca gaa atg gca cga gcc acc			576
Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr			
	180	185	190
atg cgg gag cat atc caa gtc acc gga aag cta cta cta gaa caa gca			624
Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala			
	195	200	205
gtg gaa aaa tcc ggc gaa gga gct gct cag aag att tgg gat cag tac			672
Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr			
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Thr Ala Gly Val			
225			

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<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
35 40 45

Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
50 55 60

Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
65 70 75 80

Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
85 90 95

Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
100 105 110

Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
115 120 125

Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp
 130 135 140
 Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr
 145 150 155 160
 Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro
 165 170 175
 Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr
 180 185 190
 Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala
 195 200 205
 Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr
 210 215 220
 Thr Ala Gly Val
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 gtcacaaaata gtctaaattt cgggtgtacta aggtgttgct atg gtc caa aaa gat 115
 Met Val Gln Lys Asp
 1 5
 gcc cag gcc tcc cct gct acg aga aaa gca gat cag gta tac aca cag 163
 Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp Gln Val Tyr Thr Gln
 10 15 20
 att cgt cgt gaa atc gaa gat gga acc tta aat cct ggg caa cga atg 211
 Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn Pro Gly Gln Arg Met
 25 30 35
 tcg gaa gtg tgg ctg gtt gaa cac acc ggc gct tcg aga acc cca gtc 259
 Ser Glu Val Trp Leu Val Glu His Thr Gly Ala Ser Arg Thr Pro Val
 40 45 50
 cgg gat gct ctc cgc cgg tta gcc gca gac gag ttg atc att ttg gag 307
 Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu Leu Ile Ile Leu Glu
 55 60 65
 cca cgt cag gcg cct atg gtg tgc cca ctt tgc ctt cgc cac att aag 355
 Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser Leu Arg His Ile Lys
 70 75 80 85
 gat ctg ttt gag ttc cgc agg atc gtc gag gtc gca gcg ctt gag gaa 403
 Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val Ala Ala Leu Glu Glu

90										95										100										
atc	tct	gtt	gga	gcg	agt	aaa	tca	ccg	cgt	atc	ttt	ggt	gag	ttt	tct	451														
Ile	Ser	Val	Gly	Ala	Ser	Lys	Ser	Pro	Arg	Ile	Phe	Gly	Glu	Phe	Ser															
			105						110				115																	
acg	ttg	gcg	gca	gat	ttt	cga	gag	ctg	gaa	aac	tct	gca	gac	gat	gca	499														
Thr	Leu	Ala	Ala	Asp	Phe	Arg	Glu	Leu	Glu	Asn	Ser	Ala	Asp	Asp	Ala															
		120					125					130																		
gat	ttc	acc	gcc	gat	ttt	agg	cga	ttg	acc	agt	aag	ttt	gat	gat	ctt	547														
Asp	Phe	Thr	Ala	Asp	Phe	Arg	Arg	Leu	Thr	Ser	Lys	Phe	Asp	Asp	Leu															
	135					140					145																			
gtt	gca	gca	aat	act	cac	aac	caa	ttc	ctt	gga	cgc	agc	atc	tta	agt	595														
Val	Ala	Ala	Asn	Thr	His	Asn	Gln	Phe	Leu	Gly	Arg	Ser	Ile	Leu	Ser															
150					155					160					165															
tta	aaa	ccg	cac	acc	acg	agg	ctg	cgg	atc	att	gcg	cat	tcc	gat	cat	643														
Leu	Lys	Pro	His	Thr	Thr	Arg	Leu	Arg	Ile	Ile	Ala	His	Ser	Asp	His															
				170					175					180																
gcg	cgt	ctg	cgc	caa	tcg	gtt	cag	gaa	cat	att	gaa	atg	tgt	gaa	gct	691														
Ala	Arg	Leu	Arg	Gln	Ser	Val	Gln	Glu	His	Ile	Glu	Met	Cys	Glu	Ala															
			185					190					195																	
gtg	gcc	tca	gga	gat	tta	agg	tcg	gca	ggc	gct	gcg	tgt	aga	cag	cac	739														
Val	Ala	Ser	Gly	Asp	Leu	Arg	Ser	Ala	Gly	Ala	Ala	Cys	Arg	Gln	His															
		200					205					210																		
ctg	atc	cat	gta	gaa	aag	agc	att	ttg	acc	gca	ttg	att	aat	gct	gat	787														
Leu	Ile	His	Val	Glu	Lys	Ser	Ile	Leu	Thr	Ala	Leu	Ile	Asn	Ala	Asp															
	215					220					225																			
tct	acg	ggc	tcg	cag	ggc	att	gat	att	agg	tct	tagaaccagc gtgcactgat				840															
Ser	Thr	Gly	Ser	Gln	Gly	Ile	Asp	Ile	Arg	Ser																				
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Gln	Val	Tyr	Thr	Gln	Ile	Arg	Arg	Glu	Ile	Glu	Asp	Gly	Thr	Leu	Asn															
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Pro	Gly	Gln	Arg	Met	Ser	Glu	Val	Trp	Leu	Val	Glu	His	Thr	Gly	Ala															
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Ser	Arg	Thr	Pro	Val	Arg	Asp	Ala	Leu	Arg	Arg	Leu	Ala	Ala	Asp	Glu															
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Leu	Ile	Ile	Leu	Glu	Pro	Arg	Gln	Ala	Pro	Met	Val	Ser	Pro	Leu	Ser															
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aagtgcctag	gtgtgtcccc	agtcctttaa	gatcagtcac	atg	acg	cag	gca	ata	115							
				Met	Thr	Gln	Ala	Ile								
				1				5								
gca	gca	tcc	ctt	gat	tta	gcg	gct	cga	atc	acc	gcc	aaa	att	gat	caa	163
Ala	Ala	Ser	Leu	Asp	Leu	Ala	Ala	Arg	Ile	Thr	Ala	Lys	Ile	Asp	Gln	
				10				15						20		
gga	gtg	ctc	act	cca	ggg	act	cga	cta	ccc	gag	gtt	gct	ttg	gca	gaa	211
Gly	Val	Leu	Thr	Pro	Gly	Thr	Arg	Leu	Pro	Glu	Val	Ala	Leu	Ala	Glu	
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gaa	ctt	ggc	gtt	tca	cgg	aac	acg	ctg	cgt	gaa	gct	ttt	cgg	gta	ctc	259

<400> 134
Met Thr Gln Ala Ile Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr
1 5 10 15
Ala Lys Ile Asp Gln Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu
20 25 30
Val Ala Leu Ala Glu Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu

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<211> 819
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02494
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								Met	Thr	Arg	Ile	Leu					
								1				5					
atc	gtt	gaa	gat	gag	gaa	tcg	tta	gca	gat	cct	ttg	gcc	ttt	ctt	ctt	163	
Ile	Val	Glu	Asp	Glu	Glu	Ser	Leu	Ala	Asp	Pro	Leu	Ala	Phe	Leu	Leu		
				10					15					20			
cgc	aaa	gaa	ggt	ttt	gac	acc	atc	atc	gcc	ggt	gat	ggc	cca	acc	gca	211	
Arg	Lys	Glu	Gly	Phe	Asp	Thr	Ile	Ile	Ala	Gly	Asp	Gly	Pro	Thr	Ala		
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<210> 136
<211> 232
<212> PRT
<213> Corynebacterium glutamicum
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<400> 136
Met Thr Arg Ile Leu Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro
1 5 10 15


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gcc caa cta atc gct gat gat gaa gca gta att ttc gac aac ggc acc 163
Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile Phe Asp Asn Gly Thr
      10                      15                      20

acc tgc cag gca gtg gcc caa gag ttg gcg ggg cgt ccc atc acg gca 211
Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly Arg Pro Ile Thr Ala
      25                      30                      35

ttg tgt ctg tct cta cat tcg gcg gtc gcc ctg gga agc cga gct ggc 259
Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu Gly Ser Arg Ala Gly
      40                      45                      50

acc aac gtt ttc atc ccc ggc ggc ccc gtg gaa aac gac tca ctc gcc 307
Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu Asn Asp Ser Leu Ala
      55                      60                      65

tta tct ggc ccg gct gtg atc acc gcg tta cga gat ttc tcc gcc gat 355
Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg Asp Phe Ser Ala Asp
      70                      75                      80                      85

gtc gtg atc ctc ggt tcc tgc tct aca tca ctg gag cac ggg ttg gcc 403
Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu Glu His Gly Leu Ala
      90                      95                      100

acc act acc tac gac gat gcg gaa aac aag cgc gca gcc atc cat gct 451
Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg Ala Ala Ile His Ala
      105                      110                      115

gcc acc cga cga atc ctt gtg gtg tcc gcc cgt aaa ctc aac cac gtt 499
Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg Lys Leu Asn His Val
      120                      125                      130

tcc act ttc cgt ttc gca gac gtc gcg gac tta cac cag ctg gtc aca 547
Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu His Gln Leu Val Thr
      135                      140                      145

acc tcc gat gcg cca cgg gag att ctc gcc gag atc cgg gat ctc ggc 595
Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu Ile Arg Asp Leu Gly
      150                      155                      160                      165

gtg cag gtt att act gtt ccc gcc cct gac gag caa cga agt 637
Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu Gln Arg Ser
      170                      175

taactcttca tggttgctga gca 660

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<210> 138

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Leu Ala Gln Ala Thr Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile
  1                      5                      10                      15

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Phe Asp Asn Gly Thr Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly
  20                      25                      30

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Arg Pro Ile Thr Ala Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu
  35                      40                      45

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Gly Ser Arg Ala Gly Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu
 50 55 60
 Asn Asp Ser Leu Ala Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg
 65 70 75 80
 Asp Phe Ser Ala Asp Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu
 85 90 95
 Glu His Gly Leu Ala Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg
 100 105 110
 Ala Ala Ile His Ala Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg
 115 120 125
 Lys Leu Asn His Val Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu
 130 135 140
 His Gln Leu Val Thr Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu
 145 150 155 160
 Ile Arg Asp Leu Gly Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu
 165 170 175
 Gln Arg Ser

<210> 139
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(739)
 <223> RXA00655

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 Val Ala Ala Ser Ala 5
 1
 tca ggc aag agt aaa aca agt gcc ggg gca aac cgt cgt cgc aat cga 163
 Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn Arg Arg Arg Asn Arg 20
 10 15
 cca agc ccc cga cag cgt ctc ctc gat agc gca acc aac ctt ttc acc 211
 Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala Thr Asn Leu Phe Thr 35
 25 30
 aca gaa ggt att cgc gtc atc ggt att gat cgt atc ctc cgt gaa gct 259
 Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg Ile Leu Arg Glu Ala 50
 40 45
 gac gtg gcg aag gcg agc ctc tat tcc ctt ttc gga tcg aag gac gcc 307
 Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe Gly Ser Lys Asp Ala 65
 55 60

ttg gtt att gca tac ctg gag aac ctc gat cag ctg tgg cgt gaa gcg 355
 Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln Leu Trp Arg Glu Ala
 70 75 80 85
 tgg cgt gag cgc acc gtc ggt atg aag gat ccg gaa gat aaa atc atc 403
 Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro Glu Asp Lys Ile Ile
 90 95 100
 gcg ttc ttt gat cag tgc att gag gaa gaa cca gaa aaa gat ttc cgc 451
 Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro Glu Lys Asp Phe Arg
 105 110 115
 ggc tcg cac ttt cag aat gcg gct agt gag tac cct cgc ccc gaa act 499
 Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr Pro Arg Pro Glu Thr
 120 125 130
 gat agc gaa aag ggc att gtt gca gca gtg tta gag cac cgc gag tgg 547
 Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu Glu His Arg Glu Trp
 135 140 145
 tgt cat aag act ctg act gat ttg ctc act gag aag aac ggc tac cca 595
 Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu Lys Asn Gly Tyr Pro
 150 155 160 165
 ggc acc acc cag gcg aat cag ctg ttg gtg ttc ctt gat ggt gga ctt 643
 Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe Leu Asp Gly Gly Leu
 170 175 180
 gct gga tct cga ttg gtc cac aac atc agt cct ctt gag acg gct cgc 691
 Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro Leu Glu Thr Ala Arg
 185 190 195
 gat ttg gct cgg cag ttg ttg tcg gct cca cct gcg gac tac tca att 739
 Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile
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 tagtttcttc attttccgaa ggg 762

<210> 140

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Ala Ala Ser Ala Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn
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Arg Arg Arg Asn Arg Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala
 20 25 30

Thr Asn Leu Phe Thr Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg
 35 40 45

Ile Leu Arg Glu Ala Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe
 50 55 60

Gly Ser Lys Asp Ala Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln
 65 70 75 80


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<210> 141
<211> 2538
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN03136
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taaaaaatccc cgaaacctcc ttggacacat cgcccacaaa																	115
												ttg	ggt	gcg	cac	tcc	
												Leu	Gly	Ala	His	Ser	
												1				5	
gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg																	163
Ala	Asn	Ser	Ile	Arg	Gly	Val	Ile	Asp	Arg	Leu	Asp	Ala	Ser	Thr	Val		
				10					15					20			
gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa																	211
Val	Ile	Val	Ala	Asp	Val	His	Trp	Ala	Asp	Val	Glu	Ser	Met	Gln	Lys		
			25					30					35				
ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc																	259
Leu	Ile	Glu	Tyr	Ser	Met	Arg	Met	Val	Ser	Gly	Arg	Phe	Ala	Leu	Ile		
		40					45					50					
atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc																	307
Met	Ile	Gly	Leu	Asp	Glu	Glu	Asn	Leu	Val	Phe	His	Asp	Glu	Val	Val		
	55					60					65						

tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt	355
Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser	
70 75 80 85	
att gaa gaa atc cgc cag ctt gcg ctt acc gat gtc cgc ggc cgc atc	403
Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile	
90 95 100	
agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac	451
Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr	
105 110 115	
ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga	499
Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg	
120 125 130	
atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg	547
Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu	
135 140 145	
ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc	595
Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val	
150 155 160 165	
gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc	643
Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly	
170 175 180	
aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg	691
Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu	
185 190 195	
ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg	739
Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu	
200 205 210	
ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg	787
Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu	
215 220 225	
gcg cag ttg cac cac aag gca gcc gaa tat tac ggc aag tgg aat caa	835
Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln	
230 235 240 245	
aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat	883
Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn	
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Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg	
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Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn	
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cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc	1027
Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile	
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Ser	Thr	Leu	Asp	Leu 330	Gly	Glu	Thr	Gly	Ile 335	Gln	Gln	Asp	Ser	Met	Leu 340	
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Gly	Tyr	Leu	Ala 345	Ile	His	Glu	Gly	Arg 350	Arg	Leu	Glu	Ala	Arg	Asn 355	Leu	
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Leu	His	Arg 360	Ala	Ser	Glu	Glu	Leu 365	Leu	Ala	Gln	His	Pro 370	Ile	Asp	Pro	
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Ile	Pro 440	Gly	Glu	Thr	Thr	Leu	His 445	Ala	Gln	Arg	Arg	His 450	Met	Ala	Met	
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Gln	Asp	Gly	Trp	Leu 490	Ala	Arg	Ser	Leu	Leu 495	Leu	Leu	Gly	Glu	Trp 500	Glu	
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Ser	Ala	Ala	Arg	Thr 505	Val	Glu	Ile	Gly 510	Leu	Ala	Arg	Ala	Glu 515	Gln	Phe	
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Gly	Ile	Arg	Phe 520	Leu	Glu	Pro	Leu 525	Leu	Leu	Trp	Ser	Gly 530	Ala	Thr	Ile	
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Ala	Thr	Ala	Arg	Gly	Asn 535	Ser	Asp 540	Leu	Ala	Arg	Asn 545	Tyr	Met	Ser	Arg	
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Leu	Ser	Thr	Asp	Gln	Asp	Ser	Phe	Ile	Val	Gln	Ser	Met	Pro	Ser	Ala	

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Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala							
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Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val							
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aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc	1939						
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu							
		600		605		610	
atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg	1987						
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr							
		615		620		625	
ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att	2035						
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile							
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gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag	2083						
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys							
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gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc	2131						
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr							
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ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg	2179						
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu							
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aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca	2227						
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala							
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gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc	2275						
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala							
		710		715		720	725
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc	2323						
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala							
		730		735		740	
ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct	2371						
Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser							
		745		750		755	
ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag	2419						
Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys							
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acc gtg gaa tac cat ctc acc cgg gtg tac aaa aag ctc gga ata cgc	2467						
Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Ile Arg							
		775		780		785	
aat cgg atg gaa ctt gcc gag gct ttg aag aag tac tca cac gac gcc	2515						
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2538

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Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
 35 40 45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
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His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
 65 70 75 80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
 85 90 95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
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Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
 115 120 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
 130 135 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
 145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
 165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
 180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
 195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
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Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr
 225 230 235 240

Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala
 245 250 255

Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly
 260 265 270

Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu
 275 280 285
 Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr
 290 295 300
 Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln
 305 310 315 320
 Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln
 325 330 335
 Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu
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 Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln
 355 360 365
 His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val
 370 375 380
 Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala
 385 390 395 400
 Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu
 405 410 415
 Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu
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 Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg
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 Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val
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 Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu
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 Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu
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 Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala
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 Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp
 515 520 525
 Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg
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 Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln
 545 550 555 560
 Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn
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 Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala
 580 585 590
 Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val

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Leu	Val	Asn	Ser	Thr	Leu	Glu	Glu	Leu	Arg	Gly	Ser	Asp	Ile	Met	Ser
625					630					635					640
Ala	His	Ala	Lys	Ile	Ala	Val	Pro	Asp	Ala	Met	Leu	Met	Ile	His	His
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Gly	Asp	Val	Lys	Lys	Gly	Phe	Lys	Arg	Phe	Asp	Asp	Ala	Leu	Asp	Met
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Ile	Asp	Pro	Leu	Thr	Leu	Pro	Tyr	Tyr	Arg	Ala	Arg	Ile	Cys	Phe	Glu
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Tyr	Gly	Gln	Ala	Leu	Arg	Arg	Gln	Gly	Gln	Arg	Arg	Arg	Ala	Asp	Glu
	690					695					700				
Gln	Phe	Ala	Arg	Ala	Ala	Ser	Leu	Phe	Gln	Asp	Met	Gly	Ala	Asp	Ala
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Met	Val	Thr	Leu	Ala	Asn	Arg	Glu	Arg	Arg	Val	Gly	Gly	Leu	Gly	Gln
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Arg	Ser	Glu	Gln	Ala	Gly	Gly	Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Ile	Ala
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Arg	Leu	Val	Ser	Ser	Gly	His	Ala	Asn	Arg	Glu	Val	Ala	Gln	Glu	Leu
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Phe	Leu	Ser	Pro	Lys	Thr	Val	Glu	Tyr	His	Leu	Thr	Arg	Val	Tyr	Lys
	770					775					780				
Lys	Leu	Gly	Ile	Arg	Asn	Arg	Met	Glu	Leu	Ala	Glu	Ala	Leu	Lys	Lys
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Tyr	Ser	His	Asp	Ala											
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 Leu Gly Ala His Ser
 1 5
 gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163
 Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val

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Val	Ile	Val	Ala	Asp	Val	His	Trp	Ala	Asp	Val	Glu	Ser	Met	Gln	Lys				
25								30				35							
ctc	atc	gaa	tat	tcc	atg	cgc	atg	gtt	tct	ggc	cgt	ttc	gca	ctc	atc	259			
Leu	Ile	Glu	Tyr	Ser	Met	Arg	Met	Val	Ser	Gly	Arg	Phe	Ala	Leu	Ile				
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atg	att	ggc	ctt	gat	gaa	gag	aac	tta	gtg	ttc	cac	gat	gag	gtg	gtc	30			
Met	Ile	Gly	Leu	Asp	Glu	Glu	Asn	Leu	Val	Phe	His	Asp	Glu	Val	Val				
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tcg	ctc	ccc	tcc	atc	gca	gac	tcc	acc	tac	gta	ttg	ccg	ccg	atg	agt	355			
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att	gaa	gaa	atc	cgc	cag	ctt	gcg	ctt	acc	gat	gtc	cgc	ggc	cgc	atc	403			
Ile	Glu	Glu	Ile	Arg	Gln	Leu	Ala	Leu	Thr	Asp	Val	Arg	Gly	Arg	Ile				
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agc	acc	acc	acc	gcc	aca	gac	atc	cag	cgc	atc	acc	ggc	ggc	atc	tac	451			
Ser	Thr	Thr	Thr	Ala	Thr	Asp	Ile	Gln	Arg	Ile	Thr	Gly	Gly	Ile	Tyr				
105								110				115							
ggg	cga	gtc	aaa	gaa	gtc	ctc	cac	tcg	gaa	tcc	ccc	gat	cac	tgg	cga	499			
Gly	Arg	Val	Lys	Glu	Val	Leu	His	Ser	Glu	Ser	Pro	Asp	His	Trp	Arg				
120								125				130							
atg	ccc	aac	cca	aat	att	ccc	atc	cca	caa	agc	tgg	cat	gcc	aac	ctg	547			
Met	Pro	Asn	Pro	Asn	Ile	Pro	Ile	Pro	Gln	Ser	Trp	His	Ala	Asn	Leu				
135								140				145							
ttg	aga	cgc	atc	acc	aac	gaa	gaa	gtc	tgg	cat	gta	cta	ctc	gcc	gtc	595			
Leu	Arg	Arg	Ile	Thr	Asn	Glu	Glu	Val	Trp	His	Val	Leu	Leu	Ala	Val				
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Ala	Val	Leu	Pro	Ser	Gly	Gly	Pro	Ile	Asp	Leu	Val	Lys	Leu	Ile	Gly				
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Asn	Asp	Pro	Thr	Gly	Met	Leu	Cys	Asp	Asp	Ala	Val	Arg	Ser	Gly	Leu				
185								190				195							
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Leu	Arg	Val	Leu	Pro	Ser	Asp	Gly	Gln	Pro	Gln	Val	Asp	Leu	Val	Leu				
200								205				210							
ccg	atc	gac	cgc	gcc	gta	ctg	caa	tca	cgc	act	ccg	ctc	aac	att	ctg	787			
Pro	Ile	Asp	Arg	Ala	Val	Leu	Gln	Ser	Arg	Thr	Pro	Leu	Asn	Ile	Leu				
215				220				225				230							
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Ala	Gln	Leu	His	His	Lys														

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Thr	Gly	His	Trp	Met	Glu	Ser	Ala	His	Ala	Leu	Ser	Leu	Ala	Ala	Asn	
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Arg	Thr	Ala	His	Gln	Glu	Glu	Ser	Asn	Lys	Tyr	Leu	Leu	Glu	Ser	Ile	
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Gly	Tyr	Leu	Ala	Ile	His	Glu	Gly	Arg	Arg	Leu	Glu	Ala	Arg	Asn	Leu	
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Leu	His	Arg	Ala	Ser	Glu	Glu	Leu	Leu	Ala	Gln	His	Pro	Ile	Asp	Pro	
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Ile	His	Gly	Pro	Arg	Met	Ala	Gln	Arg	Lys	Val	Leu	Leu	Asn	Leu	Val	
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gac	tgg	aat	cca	gaa	gaa	ctc	ctg	gtg	tgg	gct	gat	aga	gca	gtc	gca	1315
Asp	Trp	Asn	Pro	Glu	Glu	Leu	Leu	Val	Trp	Ala	Asp	Arg	Ala	Val	Ala	
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Trp	Thr	Glu	Glu	Asp	Ala	Gly	Glu	Lys	Val	Glu	Ala	Gln	Ala	Ile	Ser	
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Leu	Ile	Gly	Gln	Ser	Ile	Leu	Asp	Gly	Cys	Leu	Pro	Glu	Asp	Lys	Pro	
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Gly	Trp	Leu	Ser	Met	Val	His	Asp	Asp	Pro	Val	Thr	Ala	Arg	Gln	Lys	
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Leu	Glu	Arg	Arg	Thr	Ser	Ile	Asn	Gly	Ser	Glu	Arg	Ile	Ser	Leu	Trp	
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caa	gac	gga	tgg	ctg	gct	cgg	tcc	cta	ctg	ctg	ctc	ggc	gaa	tgg	gag	1603
Gln	Asp	Gly	Trp	Leu	Ala	Arg	Ser	Leu	Leu	Leu	Leu	Gly	Glu	Trp	Glu	
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Gly Ile Arg Phe Leu Glu Pro Leu Leu Trp Ser Gly Ala Thr Ile	
520 525 530	
gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga	1747
Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg	
535 540 545	
ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg	1795
Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala	
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Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala	
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Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val	
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Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu	
600 605 610	
atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg	1987
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr	
615 620 625	
ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att	2035
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile	
630 635 640 645	
gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag	2083
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys	
650 655 660	
gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc	2131
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr	
665 670 675	
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg	2179
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu	
680 685 690	
aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca	2227
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala	
695 700 705	
gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc	2275
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala	
710 715 720 725	
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc	2323
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala	
730 735 740	
ggg ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct	2371

Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser
 745 750 755

ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag 2419
 Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys
 760 765 770

acc gtg gaa tac 2431
 Thr Val Glu Tyr
 775

<210> 144

<211> 777

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Leu Gly Ala His Ser Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu
 1 5 10 15

Asp Ala Ser Thr Val Val Ile Val Ala Asp Val His Trp Ala Asp Val
 20 25 30

Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
 35 40 45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
 50 55 60

His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
 65 70 75 80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
 85 90 95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
 100 105 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
 115 120 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
 130 135 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
 145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
 165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
 180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
 195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
 210 215 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr

225	230	235	240
Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala	245	250	255
Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly	260	265	270
Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu	275	280	285
Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr	290	295	300
Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln	310	315	320
Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln	325	330	335
Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu	340	345	350
Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln	355	360	365
His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val	370	375	380
Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala	385	390	395
Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu	405	410	415
Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu	420	425	430
Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg	435	440	445
Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val	450	455	460
Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu	465	470	475
Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu	485	490	495
Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala	500	505	510
Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp	515	520	525
Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg	530	535	540
Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln	545	550	555
			560

Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn
 565 570 575
 Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala
 580 585 590
 Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val
 595 600 605
 His Ala Thr His Leu Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu
 610 615 620
 Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser
 625 630 635 640
 Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His
 645 650 655
 Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met
 660 665 670
 Ile Asp Pro Leu Thr Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu
 675 680 685
 Tyr Gly Gln Ala Leu Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu
 690 695 700
 Gln Phe Ala Arg Ala Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala
 705 710 715 720
 Met Val Thr Leu Ala Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln
 725 730 735
 Arg Ser Glu Gln Ala Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala
 740 745 750
 Arg Leu Val Ser Ser Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu
 755 760 765
 Phe Leu Ser Pro Lys Thr Val Glu Tyr
 770 775

<210> 145

<211> 471

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(448)

<223> RXA00593

<400> 145

ttgggtgtgat gcattcgaca gcaaattggc tgtgtgacta cacttgcgag tgtattaagt 60

attaggccgt gcatatgtag cgcatttttaa ggagattgtc atg acg tct gtg att 115

Met Thr Ser Val Ile

1

5

```

cca gag cag cgc aac aac ccc ttt tat agg gac agc gcc aca att gct 163
Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp Ser Ala Thr Ile Ala
      10                      15                      20

tcc tcg gac cac aca gag cgt ggt gag tgg gtc act cag gca aag tgt 211
Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val Thr Gln Ala Lys Cys
      25                      30                      35

cga aat ggc gac cca gat gca ttg ttt gtt cgt ggt gca gcg caa cgc 259
Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg Gly Ala Ala Gln Arg
      40                      45                      50

cga gca gca gca att tgc cgc cac tgc cct gta gcc atg cag tgc tgc 307
Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val Ala Met Gln Cys Cys
      55                      60                      65

gcc gat gcc tta gat aac aag gtg gaa ttc gga gtc tgg gga ggc ctg 355
Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly Val Trp Gly Gly Leu
      70                      75                      80                      85

acc gag cgc cag cgc cgt gca ttg ctt cga aag aag ccg cac att act 403
Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys Lys Pro His Ile Thr
      90                      95                      100

aac tgg gct gaa tat ttg gct cag ggg ggc gag atc gcc ggg gtt 448
Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu Ile Ala Gly Val
      105                      110                      115

taattaattt caagggctgg cca 471

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<210> 146

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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Met Thr Ser Val Ile Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp
  1                      5                      10                      15

Ser Ala Thr Ile Ala Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val
      20                      25                      30

Thr Gln Ala Lys Cys Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg
      35                      40                      45

Gly Ala Ala Gln Arg Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val
      50                      55                      60

Ala Met Gln Cys Cys Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly
      65                      70                      75                      80

Val Trp Gly Gly Leu Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys
      85                      90                      95

Lys Pro His Ile Thr Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu
      100                      105                      110

Ile Ala Gly Val
      115

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<400> 147																
cgagcgcgcga cgcggtggcc accgccaaagc tcattgcgga tccggactcc gatttcatgg 60																
ctgatctgga ggaagcgcgg cgcgtggata atatgggtgc atg ctg atc ggt gag 115																
Met Leu Ile Gly Glu 5																
1																
gtg tcc aag ctc agt ggg gtg agt gcg cgc atg ttg cgg cac tac gaa 163																
Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met Leu Arg His Tyr Glu 20																
10 15																
aag ctg ggt ttg gtc gag ccg aag cag tcg acg gcg ggg tat cgg gaa 211																
Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr Ala Gly Tyr Arg Glu 35																
25 30																
tac tca gaa ggc gat gtg cgc agg att ttc cat atc gaa ggt ttg cgc 259																
Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His Ile Glu Gly Leu Arg 50																
40 45																
agc ttg ggt ctt agt ttg aag cag gtt gga gac gcg ctt gag gat cca 307																
Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp Ala Leu Glu Asp Pro 65																
55 60																
gac ttt gat cct cag gca gtc att tcc gag atg att gct gag act tct 355																
Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met Ile Ala Glu Thr Ser 85																
70 75																
gcg cgg att tct atg gaa cgg gag ttg ctt gcc agg ctg aaa gcg gtg 403																
Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala Arg Leu Lys Ala Val 100																
90 95																
cgt cat gcg cag gcc tcg gat tgg gaa tcg gcg ttg gat gcg gtg cag 451																
Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala Leu Asp Ala Val Gln 115																
105 110																
att tta cgt cgc ctg cga tcg ggg gat ccg gcg caa cgt caa gcc gtg 499																
Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala Gln Arg Gln Ala Val 130																
120 125																
gcc tat gac tct gtc tct ggt aaa gaa gca gtt gcg cta gaa acc ttg 547																
Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val Ala Leu Glu Thr Leu 145																
135 140																
gtg gaa tcg gcg ctc ggt gag tcg cat ttg aac gcg gag ggg gcg ctg 595																
Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn Ala Glu Gly Ala Leu 165																
150 155 160																
tcg tgg gcg gtt gtg cag cgt ggt gag gaa gct gtt gca ttg gcg gca 643																
Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala Val Ala Leu Ala Ala 180																
170 175																

cga ggt ttg cgc tca agg gat gcg gcg gtg cgg ctg cgg gct gta agg 691
 Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg Leu Arg Ala Val Arg
 185 190 195

att gtg gcg agc gcg ccg agt gct gtt gcg gat cga gta gag tgg cta 739
 Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp Arg Val Glu Trp Leu
 200 205 210

cgg cca atg att cgc gat ccc gat gct ctc gtg cgt gct gaa act gcg 787
 Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val Arg Ala Glu Thr Ala
 215 220 225

ttg gcg ttg gga aaa tca ggc gat gag agt gca gtt gag cag ctc gtg 835
 Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala Val Glu Gln Leu Val
 230 235 240 245

tcc atg gtt ctc acc ggt ctt cgg gac gtg gag gca gcc gaa ttg ctt 883
 Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu Ala Ala Glu Leu Leu
 250 255 260

gcc gga ttt ggg gag ccc gtg cag tta gat gtg ttc aag aaa ttt gcg 931
 Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val Phe Lys Lys Phe Ala
 265 270 275

cgg acg ctg gat gat gag gaa aca atg tcc ccg acg 967
 Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro Thr
 280 285

<210> 148

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Met Leu Ile Gly Glu Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met
 1 5 10 15

Leu Arg His Tyr Glu Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr
 20 25 30

Ala Gly Tyr Arg Glu Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His
 35 40 45

Ile Glu Gly Leu Arg Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp
 50 55 60

Ala Leu Glu Asp Pro Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met
 65 70 75 80

Ile Ala Glu Thr Ser Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala
 85 90 95

Arg Leu Lys Ala Val Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala
 100 105 110

Leu Asp Ala Val Gln Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala
 115 120 125

Gln Arg Gln Ala Val Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val

130	135	140
Ala Leu Glu Thr Leu Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn 145 150 155 160		
Ala Glu Gly Ala Leu Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala 165 170 175		
Val Ala Leu Ala Ala Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg 180 185 190		
Leu Arg Ala Val Arg Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp 195 200 205		
Arg Val Glu Trp Leu Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val 210 215 220		
Arg Ala Glu Thr Ala Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala 225 230 235 240		
Val Glu Gln Leu Val Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu 245 250 255		
Ala Ala Glu Leu Leu Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val 260 265 270		
Phe Lys Lys Phe Ala Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro 275 280 285		

Thr

<210> 149
 <211> 420
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(397)
 <223> RXA00494

<400> 149
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 aaagctataa aaagtagctg acaataggga gtatttgaag atg aca ttg cct cac 115
 Met Thr Leu Pro His
 1 5
 cag ctt ccc ggg cca aat gca gac ttc tgg gac tgg cag ttg cac gga 163
 Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp Trp Gln Leu His Gly
 10 15 20
 acg tgc cgc ggc gag acc tcc gac gtg ttc tat cac ccg gac ggc gag 211
 Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr His Pro Asp Gly Glu
 25 30 35
 cgc ggt cgt gct cgc cag cgt cgg gag ctg cgc gca aag gcc atc tgt 259
 Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg Ala Lys Ala Ile Cys
 40 45 50

gca gca tgc cca gta ttg gaa tcc tgc cgc aag cat gca cta gct gta 307
 Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys His Ala Leu Ala Val
 55 60 65

gca gag cct tat gga gta tgg ggc gga ctt tca gag tcc gaa cga ctg 355
 Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser Glu Ser Glu Arg Leu
 70 75 80 85

gtt atc ctt cgc aac aac gag cgc aag caa cca gta gca gtt 397
 Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro Val Ala Val
 90 95

taaaagagca gacccggtca cca 420

<210> 150

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Met Thr Leu Pro His Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp
 1 5 10 15

Trp Gln Leu His Gly Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr
 20 25 30

His Pro Asp Gly Glu Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg
 35 40 45

Ala Lys Ala Ile Cys Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys
 50 55 60

His Ala Leu Ala Val Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser
 65 70 75 80

Glu Ser Glu Arg Leu Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro
 85 90 95

Val Ala Val

<210> 151

<211> 435

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> RXN01368

<400> 151

tcgcttgagg gaaggaaaaa ttttccaaac ctgctcgagg accaacatcc ccgatgagaa 60

cagacttaaa gtagctttga aagtgaagagg ggggagagta atg gaa gat tca gct 115
 Met Glu Asp Ser Ala
 1 5

```

ggg gac gta tct gca aag ttg aaa gca ggc cag act cgc acc gca ctg 163
Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln Thr Arg Thr Ala Leu
      10                      15                      20

gag atg act ttg gat gat ctg ttc gga gcg gtt gag caa gaa tgg cag 211
Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val Glu Gln Glu Trp Gln
      25                      30                      35

gag cag gcg ctg tgt gcg caa act gat cct gaa gca ttc ttt cca gaa 259
Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe Phe Pro Glu
      40                      45                      50

aaa ggt ggc tca act cgc gaa gcc aag cgg atc tgc cag ggc tgc ccg 307
Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Gln Gly Cys Pro
      55                      60                      65

gtt cgg gat gaa tgc cta gag ttt gct ctt gag cat gat gaa cgc ttt 355
Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu His Asp Glu Arg Phe
      70                      75                      80                      85

gga att tgg ggt ggt ctc tct gaa cgt gag cgc cgc cgc ctg aaa cgc 403
Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg Arg Arg Leu Lys Arg
      90                      95                      100

gaa att tcg taaaacttca agaccagtaa gcg 435
Glu Ile Ser

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<210> 152
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

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<400> 152
Met Glu Asp Ser Ala Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln
  1                      5                      10                      15

Thr Arg Thr Ala Leu Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val
      20                      25                      30

Glu Gln Glu Trp Gln Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu
      35                      40                      45

Ala Phe Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile
      50                      55                      60

Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu
      65                      70                      75                      80

His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg
      85                      90                      95

Arg Arg Leu Lys Arg Glu Ile Ser
      100

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<210> 153
<211> 152
<212> DNA
<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (1)..(129)

<223> FRXA01368

<400> 153

aag cgg atc tgc cag ggc tgc ccg gtt cgg gat gaa tgc cta gag ttt 48
 Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
 1 5 10 15

gct ctt gag cat gat gaa cgc ttt gga att tgg ggt ggt ctc tct gaa 96
 Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
 20 25 30

cgt gag cgc cgc cgc ctg aaa cgc gaa att tcg taaaacttca agaccagtaa 149
 Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
 35 40

gcg 152

<210> 154

<211> 43

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
 1 5 10 15

Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
 20 25 30

Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
 35 40

<210> 155

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXN00464

<400> 155

gaataaacca aagggtggac acttattcga acgggtgctt gatttaggca acttgagcaa 60

aattctgccca ttctgcctca aatcgggcta gttttgaagc atg agc gaa cgt cag 115
 Met Ser Glu Arg Gln
 1 5

ctg gaa aag tca att gag cac gcc gtc gag tta gcc cgc gaa gcc cga 163
 Leu Glu Lys Ser Ile Glu His Ala Val Glu Leu Ala Arg Glu Ala Arg
 10 15 20

aac atc gaa gtt ttt acc gga gcc gga atg agc gcc gac tcc ggg ttg 211
 Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser Ala Asp Ser Gly Leu

				25				30				35							
gaa	acg	tat	cgt	gat	gat	aaa	acc	ggg	ctg	tgg	agc	aac	gta	gat	cca	259			
Glu	Thr	Tyr	Arg	Asp	Asp	Lys	Thr	Gly	Leu	Trp	Ser	Asn	Val	Asp	Pro				
40				45				50											
caa	gcg	atg	gca	agt	atc	gat	gca	tgg	cgc	aaa	gat	cca	gag	cca	atg	307			
Gln	Ala	Met	Ala	Ser	Ile	Asp	Ala	Trp	Arg	Lys	Asp	Pro	Glu	Pro	Met				
55				60				65											
tgg	gcg	tgg	tat	cgc	tgg	cgc	gcc	ggg	gtg	gca	gct	agg	gca	gaa	ccc	355			
Trp	Ala	Trp	Tyr	Arg	Trp	Arg	Ala	Gly	Val	Ala	Ala	Arg	Ala	Glu	Pro				
70				75				80				85							
aac	gcg	ggg	cat	caa	gct	att	tcc	tac	tgg	gag	ggg	agt	gac	acc	gtc	403			
Asn	Ala	Gly	His	Gln	Ala	Ile	Ser	Tyr	Trp	Glu	Gly	Ser	Asp	Thr	Val				
				90				95				100							
gaa	cac	gtt	cac	atc	acc	acc	cag	aac	att	gac	aac	ctg	cac	gag	cga	451			
Glu	His	Val	His	Ile	Thr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	His	Glu	Arg				
105				110				115											
gct	ggc	tct	agc	gat	gtg	aca	cat	ctt	cat	ggc	agc	ttg	ttt	gaa	tac	499			
Ala	Gly	Ser	Ser	Asp	Val	Thr	His	Leu	His	Gly	Ser	Leu	Phe	Glu	Tyr				
120				125				130											
agg	tgc	tct	gat	tgt	gcg	act	cca	tgg	gaa	gac	gat	aaa	aac	tat	ccg	547			
Arg	Cys	Ser	Asp	Cys	Ala	Thr	Pro	Trp	Glu	Asp	Asp	Lys	Asn	Tyr	Pro				
135				140				145											
caa	gaa	ccc	att	gca	cgc	ctt	gct	cct	cca	caa	tgt	gaa	aag	tgc	gga	595			
Gln	Glu	Pro	Ile	Ala	Arg	Leu	Ala	Pro	Pro	Gln	Cys	Glu	Lys	Cys	Gly				
150				155				160				165							
ggg	ctg	att	aga	cca	ggt	gtg	gtg	tgg	ttt	ggt	gag	aac	ctg	ccc	gta	643			
Gly	Leu	Ile	Arg	Pro	Gly	Val	Val	Trp	Phe	Gly	Glu	Asn	Leu	Pro	Val				
170				175				180											
gaa	gag	tgg	gat	att	gca	gag	caa	cgc	atc	gca	gaa	gcc	gat	ctc	atg	691			
Glu	Glu	Trp	Asp	Ile	Ala	Glu	Gln	Arg	Ile	Ala	Glu	Ala	Asp	Leu	Met				
185				190				195											
atc	att	gtg	ggt	acc	tcc	ggg	att	gtt	cat	cct	gca	gca	gca	ctc	ccg	739			
Ile	Ile	Val	Gly	Thr	Ser	Gly	Ile	Val	His	Pro	Ala	Ala	Ala	Leu	Pro				
200				205				210											
caa	tta	gcc	caa	caa	cgc	ggc	gtt	ccc	atc	gtg	gag	atc	tcc	cca	acg	787			
Gln	Leu	Ala	Gln	Gln	Arg	Gly	Val	Pro	Ile	Val	Glu	Ile	Ser	Pro	Thr				
215				220				225											
cgc	acc	gaa	ctt	agc	cgg	atc	gca	gac	ttc	acc	tgg	atg	tcc	acc	gca	835			
Arg	Thr	Glu	Leu	Ser	Arg	Ile	Ala	Asp	Phe	Thr	Trp	Met	Ser	Thr	Ala				
230				235				240				245							
gcc	caa	gcg	cta	cca	gcg	ttg	atg	cga	ggt	ttg	agc	gcc	taacatgact			884			
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<210> 156
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 <213> Corynebacterium glutamicum

<400> 156
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 20 25 30
 Ala Asp Ser Gly Leu Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp
 35 40 45
 Ser Asn Val Asp Pro Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys
 50 55 60
 Asp Pro Glu Pro Met Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala
 65 70 75 80
 Ala Arg Ala Glu Pro Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu
 85 90 95
 Gly Ser Asp Thr Val Glu His Val His Ile Thr Thr Gln Asn Ile Asp
 100 105 110
 Asn Leu His Glu Arg Ala Gly Ser Ser Asp Val Thr His Leu His Gly
 115 120 125
 Ser Leu Phe Glu Tyr Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp
 130 135 140
 Asp Lys Asn Tyr Pro Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln
 145 150 155 160
 Cys Glu Lys Cys Gly Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly
 165 170 175
 Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala
 180 185 190
 Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly Ile Val His Pro
 195 200 205
 Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val
 210 215 220
 Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr
 225 230 235 240
 Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu
 245 250 255
 Ser Ala

<210> 157
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 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (75)..(332)

<223> FRXA00464

<400> 157

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Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp
1 5 10

gat att gca gag caa cgc atc gca gaa gcc gat ctc atg atc att gtg 158
Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val
15 20 25

ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg caa tta gcc 206
Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala
30 35 40

caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg cgc acc gaa 254
Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu
45 50 55 60

ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca gcc caa gcg 302
Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala
65 70 75

cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact gaagatgact tag 355
Leu Pro Ala Leu Met Arg Gly Leu Ser Ala
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<210> 158

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

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Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly
20 25 30

Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly
35 40 45

Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile
50 55 60

Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu
65 70 75 80

Met Arg Gly Leu Ser Ala
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<400> 159															
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Met Leu Ala Asp Leu 5															
ccc atc gcc tta aac cca cac gaa cca aca tcc atc ccc acg cag ctc 163															
Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser Ile Pro Thr Gln Leu 20															
aca gaa cag atc cgt cgt ctc gtg gcg agg gga att ctc acc cca gga 211															
Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly Ile Leu Thr Pro Gly 35															
gac ccg ctt ccc agc agt cgc tca cta tcc acc caa ttg ggg gta tcc 259															
Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr Gln Leu Gly Val Ser 50															
cgc ggc agt gtg gtg acc gct tat gac caa ttg gcc ggt gaa ggc tac 307															
Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu Ala Gly Glu Gly Tyr 65															
ctc agc acc gcc cgc ggt tcc ggt aca acg atc aac cca gat ctg cat 355															
Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile Asn Pro Asp Leu His 85															
ttg ttg aag cct gtg gaa att gag aag aag gag acg tcg aga agc gtc 403															
Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu Thr Ser Arg Ser Val 100															
ccg ccc ccg ctg ctc aac ctg agc ccc ggc gtg ccc gat acc gcg acg 451															
Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val Pro Asp Thr Ala Thr 115															
ctc gcc gat tcc gca tgg cgc gct gcg tgg cgc gaa gcc tgc gcc aag 499															
Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg Glu Ala Cys Ala Lys 130															
cca ccc acg cac tcc cct gag cag gga ctt ttg agg ctg cgg atc gag 547															
Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu Arg Leu Arg Ile Glu 145															
atc gcc gac cac ctg cgc cag atg cgt ggc ctc atg gtc gag ccg gag 595															
Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu Met Val Glu Pro Glu 165															
cag atc atc gtc acc gcc ggc gcg cgc gag ggg ctg agt ctg ctg ctg 643															
Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly Leu Ser Leu Leu Leu 180															

cgc acc atg gat gcg cct gcc cgc atc ggc gtc gaa tcg ccc ggc tac	691
Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val Glu Ser Pro Gly Tyr	
185 190 195	
ccc agc ctg cgc cgc atc ccg cag gtg ctt ggc cat gag acg atc gat	739
Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly His Glu Thr Ile Asp	
200 205 210	
gtg ccg acc gac gaa tcc ggc ctc gta ccc cgc gcg ctg ccc cac gac	787
Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg Ala Leu Pro His Asp	
215 220 225	
ctt aac gcg cta ctg gta acc cct agc cat caa tat ccc tac ggc ggc	835
Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln Tyr Pro Tyr Gly Gly	
230 235 240 245	
tcg ctg ccc gcc gat cgc cgc acc gcg cta gtc gcg tgg gct gag gca	883
Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val Ala Trp Ala Glu Ala	
250 255 260	
aac gat gcg ttg ctt att gaa gac gac ttc gat tct gag ctg cgc tac	931
Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp Ser Glu Leu Arg Tyr	
265 270 275	
gtc ggt atg ccg ctt ccg ccg ctg cgt gcg ctg gcg ccc gat cgc acg	979
Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu Ala Pro Asp Arg Thr	
280 285 290	
att ctg ctc ggc acg ttt tcc tcc gtg atc aca cca caa gtc gcc tgc	1027
Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr Pro Gln Val Ala Cys	
295 300 305	
gga tac ctc atc gcg ccg acg ccc cag gcg cgc gtg ctc gcc acg ctt	1075
Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg Val Leu Ala Thr Leu	
310 315 320 325	
cgc ggg att ctc ggc cag cca gtc ggc gcc atc acc caa cac gcg ctc	1123
Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile Thr Gln His Ala Leu	
330 335 340	
gcg tcc tac ctc gcc tca ggc gct tta cga cgc cgc acc caa cgt ttg	1171
Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg Arg Thr Gln Arg Leu	
345 350 355	
cgg cgc ctt tac cga cac cgc cgc tcc atc gtc caa gac acc ctc ggt	1219
Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val Gln Asp Thr Leu Gly	
360 365 370	
gac ctc ccg aat acg cag ctt cgc ccc atc aac ggt ggc ctc cac gca	1267
Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn Gly Gly Leu His Ala	
375 380 385	
gtt ctc ctt tgc gac aaa ccc caa gac ctc gtt gtc acc aca ctc gcc	1315
Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val Val Thr Thr Leu Ala	
390 395 400 405	
tcc cga ggc ctt aac gtc acc gcg ctt tcc cac tac tgg ggc ggc acc	1363
Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His Tyr Trp Gly Gly Thr	
410 415 420	
ggc gca gac aac ggc atc gtc ttc ggc ttc ggc tcc cac gac gaa gac	1411

Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly Ser His Asp Glu Asp
 425 430 435

acc ctc aga tgg gtg ctt gct gag atc agc gat gcg gtg tct cta ggc 1459
 Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp Ala Val Ser Leu Gly
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<210> 160

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Leu Ala Asp Leu Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser
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Ile Pro Thr Gln Leu Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly
 20 25 30

Ile Leu Thr Pro Gly Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr
 35 40 45

Gln Leu Gly Val Ser Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu
 50 55 60

Ala Gly Glu Gly Tyr Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile
 65 70 75 80

Asn Pro Asp Leu His Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu
 85 90 95

Thr Ser Arg Ser Val Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val
 100 105 110

Pro Asp Thr Ala Thr Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg
 115 120 125

Glu Ala Cys Ala Lys Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu
 130 135 140

Arg Leu Arg Ile Glu Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu
 145 150 155 160

Met Val Glu Pro Glu Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly
 165 170 175

Leu Ser Leu Leu Leu Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val
 180 185 190

Glu Ser Pro Gly Tyr Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly
 195 200 205

His Glu Thr Ile Asp Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg
 210 215 220

Ala Leu Pro His Asp Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln
 225 230 235 240

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<210> 161
<211> 786
<212> DNA
<213> Corynebacterium glutamicum
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<400> 161
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                               Val Thr Thr Pro Ala
                               1                               5

gag aac aac acc ctt aqc ccc gag acc aaa gta aqc atc act ggt cga 163

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aac	ggt	gag	ggt	cct	gat	cac	ttt	gca	gaa	cga	gta	aat	acc	aaa	ctc	211
Asn	Val	Glu	Val	Pro	Asp	His	Phe	Ala	Glu	Arg	Val	Asn	Thr	Lys	Leu	
			25					30					35			
gca	aag	att	gag	cgc	ctc	gac	cca	acg	ctg	acc	ttc	ttc	cac	ggt	gag	259
Ala	Lys	Ile	Glu	Arg	Leu	Asp	Pro	Thr	Leu	Thr	Phe	Phe	His	Val	Glu	
		40					45					50				
cta	cag	cac	gag	cca	aac	cca	cgt	cgt	gct	gac	gaa	agt	gat	cgc	att	307
Leu	Gln	His	Glu	Pro	Asn	Pro	Arg	Arg	Ala	Asp	Glu	Ser	Asp	Arg	Ile	
	55					60				65						
cag	atc	acc	gcc	acc	ggc	aag	gga	cac	atc	gcc	cga	gca	gaa	gca	aag	355
Gln	Ile	Thr	Ala	Thr	Gly	Lys	Gly	His	Ile	Ala	Arg	Ala	Glu	Ala	Lys	
70					75					80					85	
gaa	gac	agc	ttc	tac	gcg	gca	ctg	gaa	act	gca	cta	gcc	aag	atg	gag	403
Glu	Asp	Ser	Phe	Tyr	Ala	Ala	Leu	Glu	Thr	Ala	Leu	Ala	Lys	Met	Glu	
				90					95					100		
cgc	tcc	ctg	cgc	aaa	gtg	aag	gca	cgt	cgc	agc	att	tcc	cgc	tcc	ggt	451
Arg	Ser	Leu	Arg	Lys	Val	Lys	Ala	Arg	Arg	Ser	Ile	Ser	Arg	Ser	Gly	
			105					110					115			
cac	cgc	gca	cca	cta	ggc	act	ggt	gag	gtc	ggt	gca	cag	ttg	gta	gcc	499
His	Arg	Ala	Pro	Leu	Gly	Thr	Gly	Glu	Val	Gly	Ala	Gln	Leu	Val	Ala	
		120					125					130				
gag	tcc	caa	gag	gca	cgc	ggt	gcc	gat	gaa	ctg	ggc	aaa	tac	gat	ggt	547
Glu	Ser	Gln	Glu	Ala	Arg	Gly	Ala	Asp	Glu	Leu	Gly	Lys	Tyr	Asp	Val	
135						140					145					
gat	cct	tat	gca	gat	aag	gtc	gat	gac	gtc	atg	cca	ggc	cag	ggt	ggt	595
Asp	Pro	Tyr	Ala	Asp	Lys	Val	Asp	Asp	Val	Met	Pro	Gly	Gln	Val	Val	
150					155					160					165	
cgt	acc	aag	gaa	cac	cca	gca	acc	cca	atg	agt	gtg	gat	gac	gca	cta	643
Arg	Thr	Lys	Glu	His	Pro	Ala	Thr	Pro	Met	Ser	Val	Asp	Asp	Ala	Leu	
				170					175					180		
tcc	gag	atg	gaa	ttg	ggt	gga	cac	gat	ttc	tac	ctc	ttc	gtc	aac	gaa	691
Ser	Glu	Met	Glu	Leu	Val	Gly	His	Asp	Phe	Tyr	Leu	Phe	Val	Asn	Glu	
			185					190					195			
gag	acc	aac	cag	cca	tcg	gtg	gtg	tac	cgc	cga	cac	gca	ttc	gac	tat	739
Glu	Thr	Asn	Gln	Pro	Ser	Val	Val	Tyr	Arg	Arg	His	Ala	Phe	Asp	Tyr	
		200					205					210				
gga	tta	att	tcc	ctg	tcc	gat	gca	tagcaattag	ttgctaagta	ccc						786
Gly	Leu	Ile	Ser	Leu	Ser	Asp	Ala									
	215					220										

<210> 162

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Val Thr Thr Pro Ala Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val
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Ser Ile Thr Gly Arg Asn Val Glu Val Pro Asp His Phe Ala Glu Arg
 20 25 30

Val Asn Thr Lys Leu Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr
 35 40 45

Phe Phe His Val Glu Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp
 50 55 60

Glu Ser Asp Arg Ile Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala
 65 70 75 80

Arg Ala Glu Ala Lys Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala
 85 90 95

Leu Ala Lys Met Glu Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser
 100 105 110

Ile Ser Arg Ser Gly His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly
 115 120 125

Ala Gln Leu Val Ala Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu
 130 135 140

Gly Lys Tyr Asp Val Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met
 145 150 155 160

Pro Gly Gln Val Val Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser
 165 170 175

Val Asp Asp Ala Leu Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr
 180 185 190

Leu Phe Val Asn Glu Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg
 195 200 205

His Ala Phe Asp Tyr Gly Leu Ile Ser Leu Ser Asp Ala
 210 215 220

<210> 163

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXN02450

<400> 163

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 Met Asn Leu Lys Asp
 1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163
 Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
 10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211
 Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
 25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259
 Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
 40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307
 Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
 55 60 65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355
 Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
 70 75 80 85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403
 Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
 90 95 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451
 Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
 105 110 115

gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499
 Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
 120 125 130

ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547
 Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
 135 140 145

ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595
 Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
 150 155 160 165

gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643
 Asp Val Asp Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
 170 175 180

gca gtt ttc caa taggcaatgc gccccaatcc cct 678
 Ala Val Phe Gln
 185

<210> 164

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile
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Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser
 20 25 30

Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr
 35 40 45

Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu
 50 55 60

Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro
 65 70 75 80

Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu
 85 90 95

Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met
 100 105 110

Val Glu Asp Ala Ala Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg
 115 120 125

Leu Ser Gln Ser Val Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val
 130 135 140

Gln Phe Leu Ala Ser Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu
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Tyr Val Arg Gly Gln Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val
 165 170 175

Ala Arg Gln Trp Leu Ala Val Phe Gln
 180 185

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<211> 678

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(655)

<223> FRXA02450

<400> 165

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 Met Asn Leu Lys Asp
 1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163
 Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
 10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211
 Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
 25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259
 Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
 40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307

Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
 55 60 65
 cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355
 Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
 70 75 80 85
 tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403
 Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
 90 95 100
 gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451
 Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
 105 110 115
 gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499
 Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
 120 125 130
 ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547
 Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
 135 140 145
 ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595
 Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
 150 155 160 165
 gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643
 Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
 170 175 180
 gca gtt ttc caa taggcaatgc gcccgaatcc cct 678
 Ala Val Phe Gln
 185

<210> 166

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile
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 Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser
 20 25 30
 Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr
 35 40 45
 Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu
 50 55 60
 Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro
 65 70 75 80
 Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu
 85 90 95
 Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met

100					105					110					
Val	Glu	Asp	Ala	Ala	Val	Ala	Asp	Glu	Trp	Leu	Ser	Met	Met	Gln	Arg
		115					120					125			
Leu	Ser	Gln	Ser	Val	Pro	Glu	Leu	Val	Glu	Asn	Glu	Glu	Arg	Arg	Val
		130					135					140			
Gln	Phe	Leu	Ala	Ser	Leu	Met	Gly	Met	Asp	Arg	Asn	Phe	Tyr	Phe	Leu
		145					150					155			160
Tyr	Val	Arg	Gly	Gln	Asp	Val	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Ala	Val
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Ala	Arg	Gln	Trp	Leu	Ala	Val	Phe	Gln							
			180					185							

<210> 167
 <211> 816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(793)
 <223> RXA01898

<400> 167
 caacggcact tttgcgccca atgatcgacg ccccggtgaa ctaatccgcc tccttgatag 60
 cctcctaacg gctgtccgcg attaaggctc tgaaatacta atg agt gtg aaa gca 115
 Met Ser Val Lys Ala 5
 1
 cat gaa tct gtc atg gat tgg gtc acc gag gag ctc cgc agc ggt cgc 163
 His Glu Ser Val Met Asp Trp Val Thr Glu Glu Leu Arg Ser Gly Arg 20
 10 15
 cta aaa atc ggt gac cac ctc ccc agc gaa cgg gcg ctc tcc gaa acc 211
 Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg Ala Leu Ser Glu Thr 35
 25 30
 ctc gga gtt tcc cga agc tcc ctg cgc gag gcg ctt cgt gtg ctc gaa 259
 Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala Leu Arg Val Leu Glu 50
 40 45
 gcc ctc ggc acc att tcc acc gcc acc gga tcc ggc ccg cgg tct ggc 307
 Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser Gly Pro Arg Ser Gly 65
 55 60
 acc atc atc act gct gcc cct ggc cag gcg ctt tcc ctc tcc gtg acg 355
 Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu Ser Leu Ser Val Thr 85
 70 75 80
 ctg cag ttg gtc acc aac cag gtc ggc cac cac gat att tat gaa acc 403
 Leu Gln Leu Val Thr Asn Gln Val Gly His His Asp Ile Tyr Glu Thr 100
 90 95
 cgc caa ctc ctt gaa ggc tgg gct gcc ctg cat tcc agc gcc gaa cgt 451
 Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His Ser Ser Ala Glu Arg

105	110	115	
ggc gac tgg gac gtg gca gaa gcg ttg ctg gaa aag atg gac gac ccc Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu Lys Met Asp Asp Pro 120 125 130			499
tcg cta ccg ctc gag gat ttt ttg cgt ttc gac gcc gaa ttc cac gtt Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp Ala Glu Phe His Val 135 140 145			547
gtt atc tcc aaa ggc gcg gaa aac cct ctg atc agt acg ctc atg gaa Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile Ser Thr Leu Met Glu 150 155 160 165			595
gcc ctc cgt ttg tcc gtg gca gat cac acc gtt gcc agg gcc cgg gcg Ala Leu Arg Leu Ser Val Ala Asp His Thr Val Ala Arg Ala Arg Ala 170 175 180			643
ctc ccc gat tgg cga gcc acc tcg gcg cgt ctg cag aaa gaa cac cgc Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu Gln Lys Glu His Arg 185 190 195			691
gca atc ctc gca gca ctt cgc gca ggc gaa tcc aca gtg gcc gca acc Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser Thr Val Ala Ala Thr 200 205 210			739
ttg atc aaa gaa cac atc gaa ggc tac tac gaa gaa acc gct gcc gcc Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu Glu Thr Ala Ala Ala 215 220 225			787
gag gcc taaatgtccc gcactctgtg ggc Glu Ala 230			816

<210> 168

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met	Ser	Val	Lys	Ala	His	Glu	Ser	Val	Met	Asp	Trp	Val	Thr	Glu	Glu
1				5					10					15	

Leu	Arg	Ser	Gly	Arg	Leu	Lys	Ile	Gly	Asp	His	Leu	Pro	Ser	Glu	Arg
			20					25						30	

Ala	Leu	Ser	Glu	Thr	Leu	Gly	Val	Ser	Arg	Ser	Ser	Leu	Arg	Glu	Ala
			35				40						45		

Leu	Arg	Val	Leu	Glu	Ala	Leu	Gly	Thr	Ile	Ser	Thr	Ala	Thr	Gly	Ser
		50				55					60				

Gly	Pro	Arg	Ser	Gly	Thr	Ile	Ile	Thr	Ala	Ala	Pro	Gly	Gln	Ala	Leu
	65				70					75					80

Ser	Leu	Ser	Val	Thr	Leu	Gln	Leu	Val	Thr	Asn	Gln	Val	Gly	His	His
				85					90					95	

Asp	Ile	Tyr	Glu	Thr	Arg	Gln	Leu	Leu	Glu	Gly	Trp	Ala	Ala	Leu	His
			100				105						110		

Ser Ser Ala Glu Arg Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu
 115 120 125

Lys Met Asp Asp Pro Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp
 130 135 140

Ala Glu Phe His Val Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile
 145 150 155 160

Ser Thr Leu Met Glu Ala Leu Arg Leu Ser Val Ala Asp His Thr Val
 165 170 175

Ala Arg Ala Arg Ala Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu
 180 185 190

Gln Lys Glu His Arg Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser
 195 200 205

Thr Val Ala Ala Thr Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu
 210 215 220

Glu Thr Ala Ala Ala Glu Ala
 225 230

<210> 169
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(571)
 <223> RXA00004

<400> 169
 ttgcactgtc atgactgtat cccgcgaaga agtgtccctg ccgagccgaa ctctgaacaa 60

tgccttccgg aagtattttc caattcccga tgtaggggtca gtg ctg act caa ttg 115
 Val Leu Thr Gln Leu
 1 5

att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163
 Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
 10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211
 Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
 25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259
 Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
 40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307
 Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
 55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355
 Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe

70	75	80	85	
gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta				403
Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu	90	95	100	
gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc				451
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr	105	110	115	
att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta				499
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu	120	125	130	
aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc				547
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg	135	140	145	
cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc				594
Arg Gly Tyr Ile Asn Ser Ala Ala	150	155		

<210> 170

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser				
1	5	10	15	
Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala				
20	25	30		
Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu				
35	40	45		
Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln				
50	55	60		
Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr				
65	70	75	80	
Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile				
85	90	95		
Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg				
100	105	110		
Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser				
115	120	125		
Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro				
130	135	140		
Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala				
145	150	155		

<210> 171

<211> 418
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(418)
 <223> RXA01001

<400> 171
 tgggacaccg tgggcatgct gctcatcgtc gtggttgctg caacgatgat cgtcgatctc 60
 atctccggca ccatccgccg ccgcatcatg aagggggcta gtg acc gtg tcg tgg 115
 Val Thr Val Ser Trp
 1 5
 cac caa gca act gac gct cca cca agc atc cgc atc acc acg ctt gcg 163
 His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg Ile Thr Thr Leu Ala
 10 15 20
 cca tcg ctg cag cct aat cag cgc aaa gtc gcc gaa gtc atg ctt gtc 211
 Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala Glu Val Met Leu Val
 25 30 35
 gac gcc ccc agc atc gtc gaa ctg acc gct cag ggc ctt gca gat cgc 259
 Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln Gly Leu Ala Asp Arg
 40 45 50
 gtg ggg gtt ggg cgt gcc acc gtc atc cgc acc gcc cag tcc tta ggc 307
 Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr Ala Gln Ser Leu Gly
 55 60 65
 tac gac gga ttc ccg cag ctg cgc gtc gcc ctg gcg cag gaa ctg gca 355
 Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu Ala Gln Glu Leu Ala
 70 75 80 85
 ctg gcg cag ggc gcg tcg aga agc atg gtt gaa gga gcg tta agc tcc 403
 Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu Gly Ala Leu Ser Ser
 90 95 100
 tcg ttg ctt ggt cat 418
 Ser Leu Leu Gly His
 105

<210> 172
 <211> 106
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 172
 Val Thr Val Ser Trp His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg
 1 5 10 15
 Ile Thr Thr Leu Ala Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala
 20 25 30
 Glu Val Met Leu Val Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln
 35 40 45
 Gly Leu Ala Asp Arg Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr

50	55	60
Ala Gln Ser Leu Gly Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu		
65	70	75 80
Ala Gln Glu Leu Ala Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu		
	85	90 95
Gly Ala Leu Ser Ser Ser Leu Leu Gly His		
	100	105

<210> 173
 <211> 1578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1555)
 <223> RXA01375

<400> 173
 caagcagcca atggccgcgt atgaaaaccc ccgctccata aatacagaac acatacagaa 60
 cttgaccgac aatctaatta ccgcgaaggg ttagcagcac gtg act gaa aag tat 115
 Val Thr Glu Lys Tyr
 1 5
 cgt ccc gtc cgt gac att aag cct gct ccg gca gca atg caa tca act 163
 Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala Ala Met Gln Ser Thr
 10 15 20
 aaa caa gcg ggc cat cct gtg ttc cga agc gtt gtc gct ttt gtt tca 211
 Lys Gln Ala Gly His Pro Val Phe Arg Ser Val Val Ala Phe Val Ser
 25 30 35
 gtg ctg gtg ttg gtg gta tcg ggt ttg ggg tat ctt gct gtc gga aaa 259
 Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr Leu Ala Val Gly Lys
 40 45 50
 gtg gat ggt gtc gct tct ggc aac ttg aac ctt ggt ggc ggt cgc ggc 307
 Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu Gly Gly Gly Arg Gly
 55 60 65
 atc cag gac ggc aat gct gct gac ggt gct acc gat att ttg ttg gtg 355
 Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr Asp Ile Leu Leu Val
 70 75 80 85
 ggt tct gat tcc cgt tcc gat gct cag ggc aac acg ctg act gag gag 403
 Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn Thr Leu Thr Glu Glu
 90 95 100
 gag ctg gcg atg ctc cgc gca ggc gac gag gag aac gac aac acc gat 451
 Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu Asn Asp Asn Thr Asp
 105 110 115
 acg atc atg gtg att cgt gtt cct aac gat ggt tcc tct gcc acc gct 499
 Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly Ser Ser Ala Thr Ala
 120 125 130

gtc gcg att cct cgc gat acc tat att cat gat gac gat tac ggc aac	547
Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp Asp Asp Tyr Gly Asn	
135 140 145	
atg aag atc aac ggc gtt tac ggt gcg tac aag gat gcc cgt cgc gct	595
Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys Asp Ala Arg Arg Ala	
150 155 160 165	
gag ctc atg gaa cag ggt ttc acc aat gag tca gag ctg gaa acc cgg	643
Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser Glu Leu Glu Thr Arg	
170 175 180	
gcg aag gat gct ggc cga gaa ggt ttg atc gat gct gtg tca gat ctc	691
Ala Lys Asp Ala Gly Arg Glu Gly Leu Ile Asp Ala Val Ser Asp Leu	
185 190 195	
acc ggc atc acc gtc gat cac tac gcc gaa gtt ggc ctt ttg gga ttc	739
Thr Gly Ile Thr Val Asp His Tyr Ala Glu Val Gly Leu Leu Gly Phe	
200 205 210	
gtc ctg ctc acc gat gct gtc ggt ggt gtc gaa gtc tgc ctc aac aac	787
Val Leu Leu Thr Asp Ala Val Gly Gly Val Glu Val Cys Leu Asn Asn	
215 220 225	
gcc gtc gat gag cct tta tcc ggc gcc aac ttc cct gca ggc cgt caa	835
Ala Val Asp Glu Pro Leu Ser Gly Ala Asn Phe Pro Ala Gly Arg Gln	
230 235 240 245	
acc ctc ggt ggc tcc gat gcg ttg tct tat gtg cgc cag cgc cac gat	883
Thr Leu Gly Gly Ser Asp Ala Leu Ser Tyr Val Arg Gln Arg His Asp	
250 255 260	
ctc ccc cgc ggc gac ctc gac cgc atc gtc cgc cag cag tcg tat atg	931
Leu Pro Arg Gly Asp Leu Asp Arg Ile Val Arg Gln Gln Ser Tyr Met	
265 270 275	
gca tcg ctt gtt aat cag gtg ctg tct tct gga aca ctc acc aac cct	979
Ala Ser Leu Val Asn Gln Val Leu Ser Ser Gly Thr Leu Thr Asn Pro	
280 285 290	
gca aag ctt tcc gca ctt gct gat gcc gtc acc cgc tcc gtc gtc atc	1027
Ala Lys Leu Ser Ala Leu Ala Asp Ala Val Thr Arg Ser Val Val Ile	
295 300 305	
gac gaa ggc tgg gag atc atg agc ttt gcc act cag ctg cag aac ctc	1075
Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr Gln Leu Gln Asn Leu	
310 315 320 325	
gcg ggc ggc aac gtc aca ttt gcc acc atc ccg gtt acc tct atc gac	1123
Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro Val Thr Ser Ile Asp	
330 335 340	
ggc acc ggc gat tac ggc gag tcc gtt gtc acc atc gat gtc aac cag	1171
Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr Ile Asp Val Asn Gln	
345 350 355	
gtg cat gca ttc ttc caa gaa gca ctc ggc gaa gca gag cca gct cca	1219
Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu Ala Glu Pro Ala Pro	
360 365 370	
gaa gac ggc tcc gac gat caa tct gct gat cag gcc cct gac cta agc	1267

Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln Ala Pro Asp Leu Ser
 375 380 385
 gaa gtc gag gtc cac gtc ctc aac gct tcc tac gtc gaa ggc ctc gcc 1315
 Glu Val Glu Val His Val Leu Asn Ala Ser Tyr Val Glu Gly Leu Ala
 390 395 400 405
 aac ggt atc gcc gcg caa ctg cag gaa ttg ggt tac tcc atc gca gag 1363
 Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly Tyr Ser Ile Ala Glu
 410 415 420
 acc ggc aac gca gcg gaa ggc ctc tac tac gag tcc cag atc ctc gcc 1411
 Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu Ser Gln Ile Leu Ala
 425 430 435
 gcc gaa gaa gac agc gcc aag gcc ctc gcg att tcc gaa gcc ctc ggt 1459
 Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile Ser Glu Ala Leu Gly
 440 445 450
 ggt ctc cca tcg tgg cca act ctt ccc tcg acg aca aca ccg tca tcg 1507
 Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr Thr Thr Pro Ser Ser
 455 460 465
 tcg tat ccg ccg gcg att acg ctg gcc cta ccg cgg aag caa acg ccg 1555
 Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro Arg Lys Gln Thr Pro
 470 475 480 485
 tgacatccag caccgtcggc cag 1578

<210> 174

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Val Thr Glu Lys Tyr Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala
 1 5 10 15
 Ala Met Gln Ser Thr Lys Gln Ala Gly His Pro Val Phe Arg Ser Val
 20 25 30
 Val Ala Phe Val Ser Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr
 35 40 45
 Leu Ala Val Gly Lys Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu
 50 55 60
 Gly Gly Gly Arg Gly Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr
 65 70 75 80
 Asp Ile Leu Leu Val Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn
 85 90 95
 Thr Leu Thr Glu Glu Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu
 100 105 110
 Asn Asp Asn Thr Asp Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly
 115 120 125
 Ser Ser Ala Thr Ala Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp

130					135					140					
Asp	Asp	Tyr	Gly	Asn	Met	Lys	Ile	Asn	Gly	Val	Tyr	Gly	Ala	Tyr	Lys
145					150					155					160
Asp	Ala	Arg	Arg	Ala	Glu	Leu	Met	Glu	Gln	Gly	Phe	Thr	Asn	Glu	Ser
				165					170					175	
Glu	Leu	Glu	Thr	Arg	Ala	Lys	Asp	Ala	Gly	Arg	Glu	Gly	Leu	Ile	Asp
			180					185					190		
Ala	Val	Ser	Asp	Leu	Thr	Gly	Ile	Thr	Val	Asp	His	Tyr	Ala	Glu	Val
		195					200					205			
Gly	Leu	Leu	Gly	Phe	Val	Leu	Leu	Thr	Asp	Ala	Val	Gly	Gly	Val	Glu
	210					215					220				
Val	Cys	Leu	Asn	Asn	Ala	Val	Asp	Glu	Pro	Leu	Ser	Gly	Ala	Asn	Phe
225					230					235					240
Pro	Ala	Gly	Arg	Gln	Thr	Leu	Gly	Gly	Ser	Asp	Ala	Leu	Ser	Tyr	Val
				245					250					255	
Arg	Gln	Arg	His	Asp	Leu	Pro	Arg	Gly	Asp	Leu	Asp	Arg	Ile	Val	Arg
			260					265					270		
Gln	Gln	Ser	Tyr	Met	Ala	Ser	Leu	Val	Asn	Gln	Val	Leu	Ser	Ser	Gly
		275					280					285			
Thr	Leu	Thr	Asn	Pro	Ala	Lys	Leu	Ser	Ala	Leu	Ala	Asp	Ala	Val	Thr
	290					295					300				
Arg	Ser	Val	Val	Ile	Asp	Glu	Gly	Trp	Glu	Ile	Met	Ser	Phe	Ala	Thr
305					310					315					320
Gln	Leu	Gln	Asn	Leu	Ala	Gly	Gly	Asn	Val	Thr	Phe	Ala	Thr	Ile	Pro
			325						330					335	
Val	Thr	Ser	Ile	Asp	Gly	Thr	Gly	Asp	Tyr	Gly	Glu	Ser	Val	Val	Thr
			340					345					350		
Ile	Asp	Val	Asn	Gln	Val	His	Ala	Phe	Phe	Gln	Glu	Ala	Leu	Gly	Glu
		355					360					365			
Ala	Glu	Pro	Ala	Pro	Glu	Asp	Gly	Ser	Asp	Asp	Gln	Ser	Ala	Asp	Gln
	370					375					380				
Ala	Pro	Asp	Leu	Ser	Glu	Val	Glu	Val	His	Val	Leu	Asn	Ala	Ser	Tyr
385					390					395					400
Val	Glu	Gly	Leu	Ala	Asn	Gly	Ile	Ala	Ala	Gln	Leu	Gln	Glu	Leu	Gly
			405						410					415	
Tyr	Ser	Ile	Ala	Glu	Thr	Gly	Asn	Ala	Ala	Glu	Gly	Leu	Tyr	Tyr	Glu
			420				425						430		
Ser	Gln	Ile	Leu	Ala	Ala	Glu	Glu	Asp	Ser	Ala	Lys	Ala	Leu	Ala	Ile
		435					440					445			
Ser	Glu	Ala	Leu	Gly	Gly	Leu	Pro	Ser	Trp	Pro	Thr	Leu	Pro	Ser	Thr
	450					455					460				

Thr Thr Pro Ser Ser Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro
 465 470 475 480

Arg Lys Gln Thr Pro
 485

<210> 175
 <211> 508
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(508)
 <223> RXA02831

<400> 175
 cgaactggcg cgtgtcttgt ccgacgcagc ctagcccgcc tttattgacc cctccggcac 60

gcttcgatag ggctaggaaa accctgtcgg aggagcgccc atg aca cat cgg atc 115
 Met Thr His Arg Ile
 1 5

aca ccc gaa ctc tcg gcc gaa ttg cgg ggg gtg gcc cac agc ctt gca 163
 Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val Ala His Ser Leu Ala
 10 15 20

gat gcg gcg cgg ccc gtc acc ttg caa tac ttc cgc aca gca gtc gcg 211
 Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe Arg Thr Ala Val Ala
 25 30 35

gca gat aac aaa ggc gcg ctg cgc ggg atg gct tac gac ccc gtc acc 259
 Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala Tyr Asp Pro Val Thr
 40 45 50

att gcc gac cgt gca agc gaa cag gcc atg cgt gac att ctg gcc cgt 307
 Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg Asp Ile Leu Ala Arg
 55 60 65

cta cgc ccc gat gat gcg atc ttg ggt gaa gaa ttc ggc ccc aaa gcg 355
 Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu Phe Gly Pro Lys Ala
 70 75 80 85

ggc aca acg ggc ctc aca tgg gtg ctg gac ccg att gac ggc act cgc 403
 Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Arg
 90 95 100

gca tat atc gcg ggc gcg ccc act tgg ggc gtg ctg atc gca gta tcg 451
 Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val Leu Ile Ala Val Ser
 105 110 115

gat gat cag ggc ccg ctg ttc ggt atc gtc gac caa ccc tat att ggc 499
 Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp Gln Pro Tyr Ile Gly
 120 125 130

gag cgt ttt 508
 Glu Arg Phe
 135

<210> 176
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 176
 Met Thr His Arg Ile Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val
 1 5 10 15
 Ala His Ser Leu Ala Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe
 20 25 30
 Arg Thr Ala Val Ala Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala
 35 40 45
 Tyr Asp Pro Val Thr Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg
 50 55 60
 Asp Ile Leu Ala Arg Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu
 65 70 75 80
 Phe Gly Pro Lys Ala Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro
 85 90 95
 Ile Asp Gly Thr Arg Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val
 100 105 110
 Leu Ile Ala Val Ser Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp
 115 120 125
 Gln Pro Tyr Ile Gly Glu Arg Phe
 130 135

<210> 177
 <211> 696
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(673)
 <223> RXA01110

<400> 177
 atcatcgaca tgctccggaa aacttaaaaa ttcccggacg gttcacgcag attaccctag 60
 caaagcaatc tagctgacga cccaatatag tcctgtcatt atg ctg gca att gtg 115
 Met Leu Ala Ile Val
 1 5
 cag cta tca aaa gaa tct att att ggc gca gcc gtt tcg atc ttg agc 163
 Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala Val Ser Ile Leu Ser
 10 15 20
 gaa ttc ggt ttg tcg gat atg acc atg cgc cgc gtc gca aag cag tta 211
 Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg Val Ala Lys Gln Leu
 25 30 35
 aat gtc gcg ccg ggc gcg ctg tat tgg cat ttt aaa aat aag cag gag 259

Asn	Val	Ala	Pro	Gly	Ala	Leu	Tyr	Trp	His	Phe	Lys	Asn	Lys	Gln	Glu		
		40					45					50					
ctt	atc	gac	gcc	acc	tcg	cgc	tat	ctc	ctc	gcg	cct	gtc	ttg	ggg	cgc	307	
Leu	Ile	Asp	Ala	Thr	Ser	Arg	Tyr	Leu	Leu	Ala	Pro	Val	Leu	Gly	Arg		
	55					60					65						
aac	gac	gag	cag	cga	gca	agc	att	tcc	gcg	cag	gaa	acc	tgc	gcg	gaa	355	
Asn	Asp	Glu	Gln	Arg	Ala	Ser	Ile	Ser	Ala	Gln	Glu	Thr	Cys	Ala	Glu		
	70				75					80					85		
atg	cgt	tcg	ctg	atg	atg	caa	acc	aaa	gat	ggg	gcg	gaa	gtc	atc	agt	403	
Met	Arg	Ser	Leu	Met	Met	Gln	Thr	Lys	Asp	Gly	Ala	Glu	Val	Ile	Ser		
				90					95					100			
gcc	gca	ctg	agt	aat	cag	caa	ttg	cgc	caa	gaa	ttg	gaa	tca	ctc	att	451	
Ala	Ala	Leu	Ser	Asn	Gln	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	Ile		
			105					110					115				
tct	gac	tct	tta	aag	gaa	cct	aat	gag	gtt	ggc	gct	ttt	acg	ctg	cta	499	
Ser	Asp	Ser	Leu	Lys	Glu	Pro	Asn	Glu	Val	Gly	Ala	Phe	Thr	Leu	Leu		
		120					125					130					
cat	ttt	gtg	gtg	ggg	gca	gta	tta	aca	gaa	caa	act	cag	ctg	cag	atg	547	
His	Phe	Val	Val	Gly	Ala	Val	Leu	Thr	Glu	Gln	Thr	Gln	Leu	Gln	Met		
	135					140						145					
cac	gag	ttc	acg	gct	ggc	gcg	gga	gat	gac	acg	caa	gaa	aac	cct	gcc	595	
His	Glu	Phe	Thr	Ala	Gly	Ala	Gly	Asp	Asp	Thr	Gln	Glu	Asn	Pro	Ala		
	150				155					160					165		
gat	gca	aac	ttt	gag	gag	aga	ttc	aat	caa	gga	ata	gaa	atc	att	ctg	643	
Asp	Ala	Asn	Phe	Glu	Glu	Arg	Phe	Asn	Gln	Gly	Ile	Glu	Ile	Ile	Leu		
				170					175					180			
gtg	ggg	cta	gac	gcg	ctt	ggg	cat	ata	aga	tgacgttcca	tgacatcaac	gat	696				
Val	Gly	Leu	Asp	Ala	Leu	Gly	His	Ile	Arg								
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<210> 178

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

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Val	Ala	Lys	Gln	Leu	Asn	Val	Ala	Pro	Gly	Ala	Leu	Tyr	Trp	His	Phe		
		35					40					45					
Lys	Asn	Lys	Gln	Glu	Leu	Ile	Asp	Ala	Thr	Ser	Arg	Tyr	Leu	Leu	Ala		
	50					55					60						
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cgctggttgt cttgtagaaa aaggcgtaac gtcataataac atg cct agc gaa act 115															
Met Pro Ser Glu Thr 5															
atg aaa cca gcc gta gcg tca act ctg gcg gcc act tcc acg gga cgt 163															
Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala Thr Ser Thr Gly Arg 20															
cgt cct gga cgc ccc acc caa cgt atc ctt tcc gtc gaa tcc ata gtg 211															
Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser Val Glu Ser Ile Val 35															
gag cgc act tta aac att gcc ggc cgc gaa gga ttc gct gcc gtg acc 259															
Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly Phe Ala Ala Val Thr 40															
atg aac cgc ctc gcc cga gac atg ggt gtc acc cct cgc gca ctg tat 307															
Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr Pro Arg Ala Leu Tyr 55															
aac cat gtg cta aat cgt caa gaa atc att gat cgc gtc tgg gtg cgc 355															
Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp Arg Val Trp Val Arg 70															
atc atc gat gat atc aag gtg ccc gat ctt gat ccg gac aat tgg cgg 403															

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20 25 30
Val Glu Ser Ile Val Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly
35 40 45
Phe Ala Ala Val Thr Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr
50 55 60

Pro Arg Ala Leu Tyr Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp
 65 70 75 80
 Arg Val Trp Val Arg Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp
 85 90 95
 Pro Asp Asn Trp Arg Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg
 100 105 110
 Asp Gln Phe Arg Glu Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu
 115 120 125
 Gln Ile Ser Thr Gln Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu
 130 135 140
 Glu Ser Leu Lys Phe Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala
 145 150 155 160
 Thr Ile Ile Arg Glu Met Met Met Ala Asp Val Phe Ser Phe Thr Leu
 165 170 175
 Thr Ser Asp Tyr Thr Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp
 180 185 190
 Val Phe Ala Pro Val Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val
 195 200 205
 Glu Ala Pro Leu Thr Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser
 210 215 220
 Asp Glu Leu Phe Gly Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu
 225 230 235 240
 Lys Leu Leu Ala Ala Lys
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 <223> RXA01118

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 Met Val Glu Gln Ser 5
 cca gat ttc gta caa tca ttt gcc cgc ggc tta tct gtg atc cga agt 163
 Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu Ser Val Ile Arg Ser 20
 ttc agc gca gat aat cca tcg caa aca ctg tcc gaa gtc gcc agc caa 211
 Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser Glu Val Ala Ser Gln

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act	gga	ctc	tca	agg	gcc	acc	gct	agg	cgc	ttt	ctc	cac	acc	ttg	acc	259														
Thr	Gly	Leu	Ser	Arg	Ala	Thr	Ala	Arg	Arg	Phe	Leu	His	Thr	Leu	Thr															
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gac	ctt	gga	tat	gcg	gta	aac	aac	gat	tcc	cgg	ttc	cag	ctc	aca	cca	307														
Asp	Leu	Gly	Tyr	Ala	Val	Asn	Asn	Asp	Ser	Arg	Phe	Gln	Leu	Thr	Pro															
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Arg	Val	Leu	Glu	Leu	Gly	Ala	Ser	Tyr	Leu	Ser	Ala	Leu	Ser	Leu	Pro															
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Ala	Ile	Ala	Gln	Pro	Arg	Leu	Glu	Val	Leu	Ser	Arg	Gln	Val	Gly	Glu															
90					95					100																				
tca	agc	tcc	atg	tcc	gta	ctc	gac	ggc	act	gac	atc	atc	tac	gtt	tgc	451														
Ser	Ser	Ser	Met	Ser	Val	Leu	Asp	Gly	Thr	Asp	Ile	Ile	Tyr	Val	Cys															
105					110					115																				
cgc	gtt	ccg	gtg	cgc	cgc	atc	atg	acg	gtg	aac	atc	acc	atc	ggc	acc	499														
Arg	Val	Pro	Val	Arg	Arg	Ile	Met	Thr	Val	Asn	Ile	Thr	Ile	Gly	Thr															
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cgt	ttc	cct	gcg	tac	gcc	acc	tcc	atg	gga	cgc	atc	atg	ctg	gcc	aac	547														
Arg	Phe	Pro	Ala	Tyr	Ala	Thr	Ser	Met	Gly	Arg	Ile	Met	Leu	Ala	Asn															
135					140					145																				
ctt	ccc	gaa	gaa	gaa	tta	gat	gaa	atg	ctg	gcg	gcg	gca	ccc	cct	gaa	595														
Leu	Pro	Glu	Glu	Glu	Leu	Asp	Glu	Met	Leu	Ala	Ala	Ala	Pro	Pro	Glu															
150					155					160					165															
cag	ttg	acc	acc	cgg	tca	ctg	acc	tcc	atc	gcc	tca	atc	cgg	gaa	gag	643														
Gln	Leu	Thr	Thr	Arg	Ser	Leu	Thr	Ser	Ile	Ala	Ser	Ile	Arg	Glu	Glu															
170					175					180																				
atc	att	gct	acc	cgc	gaa	agg	ggg	tgg	tca	ttg	gtg	gat	cag	gag	ctc	691														
Ile	Ile	Ala	Thr	Arg	Glu	Arg	Gly	Trp	Ser	Leu	Val	Asp	Gln	Glu	Leu															
185					190					195																				
gag	ccg	ggc	ctg	cgt	tcg	ctc	gcg	gcg	ccg	atc	acc	aat	gcc	cag	ggc	739														
Glu	Pro	Gly	Leu	Arg	Ser	Leu	Ala	Ala	Pro	Ile	Thr	Asn	Ala	Gln	Gly															
200					205					210																				
gaa	gtg	gtt	gct	tcc	atc	aat	gtg	tcg	acc	caa	tcg	gca	tca	cat	tcg	787														
Glu	Val	Val	Ala	Ser	Ile	Asn	Val	Ser	Thr	Gln	Ser	Ala	Ser	His	Ser															
215					220					225																				
gtg	gaa	gat	atc	cgc	aag	ctg	gtg	ctg	ccg	cag	ctt	tta	gaa	acg	gct	835														
Val	Glu	Asp	Ile	Arg	Lys	Leu	Val	Leu	Pro	Gln	Leu	Leu	Glu	Thr	Ala															
230					235					240					245															
caa	gca	att	tcg	aca	gat	ctc	tct	gca	ctc	ttaa	taagg	atcaaaaa	aat	gaa	888															
Gln	Ala	Ile	Ser	Thr	Asp	Leu	Ser	Ala	Leu																					
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<211> 255

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 182

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Glu Val Ala Ser Gln Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe
 35           40           45

Leu His Thr Leu Thr Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg
 50           55           60

Phe Gln Leu Thr Pro Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser
 65           70           75           80

Ala Leu Ser Leu Pro Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser
           85           90           95

Arg Gln Val Gly Glu Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp
 100          105          110

Ile Ile Tyr Val Cys Arg Val Pro Val Arg Arg Ile Met Thr Val Asn
 115          120          125

Ile Thr Ile Gly Thr Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg
 130          135          140

Ile Met Leu Ala Asn Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala
 145          150          155          160

Ala Ala Pro Pro Glu Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala
 165          170          175

Ser Ile Arg Glu Glu Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu
 180          185          190

Val Asp Gln Glu Leu Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile
 195          200          205

Thr Asn Ala Gln Gly Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln
 210          215          220

Ser Ala Ser His Ser Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln
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Leu Leu Glu Thr Ala Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
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<211> 654

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(654)

<223> RXA01840

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Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly	
20 25 30	
tgg acc tcc gcc tcc cgc aaa gca atg ctc ccc gtc ttt gag ggc aat	144
Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn	
35 40 45	
aac tcc ctg ctg ttc tac ccg gtg cag tac gag ggc atg gaa tcc tcg	192
Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser	
50 55 60	
ccg aat att ttc tac acc ggc gcc acc acc aac cag cag atc atc ccg	240
Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro	
65 70 75 80	
gct ctt gat tac ctg cgt gaa aac ggc ctg aac cgc ctt ttc ctt gtc	288
Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val	
85 90 95	
ggt tcc gat tat gtt ttc cca cgc act gca aat tcc atc atc aag gac	336
Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp	
100 105 110	
tac gcc gaa gcc aat ggt atg gaa atc gtc ggc gaa gac tac gcg ccg	384
Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro	
115 120 125	
ttg gga tcc acc gac ttc acc acc atc gcc aac cgc atg cgt gac tcc	432
Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser	
130 135 140	
aac gca gat gcc gtg ttc aac act ttg aat ggc gat tcc aac gtg gcg	480
Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala	
145 150 155 160	
ttc ttc cgc cag tac aac agc ctc ggc ttc aat gca gac acc ctt ccg	528
Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro	
165 170 175	
gtg atg tca gta tcc att gcg gaa gaa gaa gtc gga ggc atc ggc acc	576
Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr	
180 185 190	
gca aat att gag ggc cag ctg gtg gcg tgg gac tac tac caa acc atc	624
Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile	
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gac acc cca gaa aac gag acc ttc gtg gag	654
Asp Thr Pro Glu Asn Glu Thr Phe Val Glu	
210 215	

<210> 184
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184
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 35 40 45
 Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser
 50 55 60
 Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro
 65 70 75 80
 Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val
 85 90 95
 Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp
 100 105 110
 Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro
 115 120 125
 Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser
 130 135 140
 Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala
 145 150 155 160
 Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro
 165 170 175
 Val Met Ser Val Ser Ile Ala Glu Glu Glu Val Gly Gly Ile Gly Thr
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 Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile
 195 200 205
 Asp Thr Pro Glu Asn Glu Thr Phe Val Glu
 210 215

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 <223> RXA00400

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	Leu Phe Thr Leu Glu	
	1 5	
cag ttg cgg tgt ttt gtc gcc gtc gcc aat cat ctt cat ttc gga aaa	163	
Gln Leu Arg Cys Phe Val Ala Val Ala Asn His Leu His Phe Gly Lys		
	10 15 20	
gct gct gca gag cta tcc atg acg cag ccg ccg ttg agt cgt cag att	211	
Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro Leu Ser Arg Gln Ile		
	25 30 35	
caa aag ctg gag aag atc gtc ggt gca acc ctg ctt gat cgt gac aac	259	
Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu Leu Asp Arg Asp Asn		
	40 45 50	
cgc aag gtg gaa ctg acc act gcg ggt ttc gca ttt ttg aag gat gct	307	
Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala Phe Leu Lys Asp Ala		
	55 60 65	
cgc ctc att ctc aat tcc acc gag aag gcg gct gag cgc gca cga ttg	355	
Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala Glu Arg Ala Arg Leu		
	70 75 80 85	
gct agc tct ggc atg tgg gga cag ctc aat att gga tac acc gct gca	403	
Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile Gly Tyr Thr Ala Ala		
	90 95 100	
gcg ggt ttt tcc att ctg ggc ccg acg ttg aat cag ttg cat gag aag	451	
Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn Gln Leu His Glu Lys		
	105 110 115	
atg ccg ggg gtc agt gtc gat ctt ttt gag atg gtc tcc acc gag cag	499	
Met Pro Gly Val Ser Val Asp Leu Phe Glu Met Val Ser Thr Glu Gln		
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atc gcc gcc ttg gaa tct ggg cta ctg gat ctt ggc att ggc cga ttg	547	
Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu Gly Ile Gly Arg Leu		
	135 140 145	
agc tcg cca gtt gag ggt ctt caa act cga cgt ctc cag gca gat tcc	595	
Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg Leu Gln Ala Asp Ser		
	150 155 160 165	
ttg gtt ctt gca gct ccg aag ggg cat cca ctt ctt gat cag aat cga	643	
Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu Leu Asp Gln Asn Arg		
	170 175 180	
cca ctg ttg cgg aag cat ctg act ggg gtt cct ttt ctg cag cac tct	691	
Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro Phe Leu Gln His Ser		
	185 190 195	
ccc acc aag gcg aag tac ctc tac gac atc gtt gtt aga aac ttc acg	739	
Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val Val Arg Asn Phe Thr		
	200 205 210	
atc aat gat gcg cag gtg caa cat acg ctg agc cag atc acc acg atg	787	
Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser Gln Ile Thr Thr Met		
	215 220 225	

gtt agt ctg gtg gcc tct gga ctg ggt gtt gcg ctg gtt ccg gag tct 835
 Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala Leu Val Pro Glu Ser
 230 235 240 245
 gcg aaa aaa ctc aat tac agc ggt gtt gag tat cgc cat ttt tat gat 883
 Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr Arg His Phe Tyr Asp
 250 255 260
 cta cct gtt ggt tta gcg gag ctg cag gct att tat tcc acc tcg aat 931
 Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile Tyr Ser Thr Ser Asn
 265 270 275
 gat aat cct gcg gtg cgg aaa ttc atc aaa aac att gac gat acc ttt 979
 Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn Ile Asp Asp Thr Phe
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<210> 186

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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 35 40 45

Leu Asp Arg Asp Asn Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala
 50 55 60

Phe Leu Lys Asp Ala Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala
 65 70 75 80

Glu Arg Ala Arg Leu Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile
 85 90 95

Gly Tyr Thr Ala Ala Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn
 100 105 110

Gln Leu His Glu Lys Met Pro Gly Val Ser Val Asp Leu Phe Glu Met
 115 120 125

Val Ser Thr Glu Gln Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu
 130 135 140

Gly Ile Gly Arg Leu Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg
 145 150 155 160

Leu Gln Ala Asp Ser Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu
 165 170 175

Leu Asp Gln Asn Arg Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro
 180 185 190

Phe Leu Gln His Ser Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val
 195 200 205
 Val Arg Asn Phe Thr Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser
 210 215 220
 Gln Ile Thr Thr Met Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala
 225 230 235 240
 Leu Val Pro Glu Ser Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr
 245 250 255
 Arg His Phe Tyr Asp Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile
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 275 280 285
 Ile Asp Asp Thr Phe
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 <223> RXA02787

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 Met Ala Gln Asp Ser
 1 5
 ctt ttt gaa acg ccc gaa aca ccg gga tcc gca ggc aac aca agc agc 163
 Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala Gly Asn Thr Ser Ser
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 gtg agc aat tcc aaa gcc gcc tcg aag tat ttt cac cca ggc gga cac 211
 Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe His Pro Gly Gly His
 25 30 35
 gca ccc ctt gct gcc cgc atg agg cca agg acg ctt gat gaa gtg gtt 259
 Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr Leu Asp Glu Val Val
 40 45 50
 ggc caa cag cat ttg ctg ggg gag ggc agg cca ctt cgc cgg ctc att 307
 Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro Leu Arg Arg Leu Ile
 55 60 65
 gaa ggt tca ggg gat gcc tcc gtc att ttg tat ggg cct ccc ggc act 355
 Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr Gly Pro Pro Gly Thr
 70 75 80 85
 gga aaa aca acc att gcc tca ttg att tct gca gct gca ggc gat cgc 403
 Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala Ala Ala Gly Asp Arg

90								95				100					
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Phe	Val	Ala	Met	Ser	Ala	Leu	Ser	Ser	Gly	Val	Lys	Glu	Val	Arg	Ala		
			105						110					115			
ggt	att	gaa	cgt	gcg	agg	atg	gat	ctg	caa	tta	ggg	cag	cgc	acc	gtg	499	
Val	Ile	Glu	Arg	Ala	Arg	Met	Asp	Leu	Gln	Leu	Gly	Gln	Arg	Thr	Val		
			120					125					130				
ctg	ttt	att	gat	gag	gtt	cat	agg	ttt	tcc	aaa	act	cag	cag	gac	gcg	547	
Leu	Phe	Ile	Asp	Glu	Val	His	Arg	Phe	Ser	Lys	Thr	Gln	Gln	Asp	Ala		
			135				140					145					
ttg	ctc	tct	gca	gtg	gaa	aac	cgc	acc	gtg	ttg	ctc	gtt	gca	gcg	acc	595	
Leu	Leu	Ser	Ala	Val	Glu	Asn	Arg	Thr	Val	Leu	Leu	Val	Ala	Ala	Thr		
						155				160					165		
act	gag	aac	ccc	tcc	ttt	tca	gtg	gtg	tct	cca	ctg	ctg	tcc	agg	tcc	643	
Thr	Glu	Asn	Pro	Ser	Phe	Ser	Val	Val	Ser	Pro	Leu	Leu	Ser	Arg	Ser		
				170					175					180			
ttg	ctg	ctc	cag	ttg	gaa	tct	tta	agc	gat	gag	gat	att	aaa	aca	gtc	691	
Leu	Leu	Leu	Gln	Leu	Glu	Ser	Leu	Ser	Asp	Glu	Asp	Ile	Lys	Thr	Val		
			185					190					195				
ctt	aat	aaa	gcg	ctt	gaa	gat	gag	cgt	gga	ctt	gcc	ggg	cga	atc	acc	739	
Leu	Asn	Lys	Ala	Leu	Glu	Asp	Glu	Arg	Gly	Leu	Ala	Gly	Arg	Ile	Thr		
			200					205					210				
gcc	acc	gat	gaa	gca	gtt	gac	cag	ttg	gtt	ctt	ctt	gcc	ggg	ggc	gat	787	
Ala	Thr	Asp	Glu	Ala	Val	Asp	Gln	Leu	Val	Leu	Leu	Ala	Gly	Gly	Asp		
			215				220					225					
gcc	cgc	cga	ggc	ctg	acc	tac	att	gaa	gcc	gct	gca	gaa	gcc	gta	gaa	835	
Ala	Arg	Arg	Gly	Leu	Thr	Tyr	Ile	Glu	Ala	Ala	Ala	Glu	Ala	Val	Glu		
			230			235				240					245		
gat	ggc	ggc	gtt	tta	gat	att	gac	acc	gtc	atg	gcc	aac	gtg	aac	cgc	883	
Asp	Gly	Gly	Val	Leu	Asp	Ile	Asp	Thr	Val	Met	Ala	Asn	Val	Asn	Arg		
				250					255					260			
gca	gtg	gtc	cgc	tat	gac	cgc	gat	ggc	gat	cag	cac	tat	gac	gtg	gtc	931	
Ala	Val	Val	Arg	Tyr	Asp	Arg	Asp	Gly	Asp	Gln	His	Tyr	Asp	Val	Val		
			265					270					275				
agt	gcc	tgg	atc	aaa	tca	att	aga	ggc	tcc	gat	gta	gac	gca	gcc	ttg	979	
Ser	Ala	Trp	Ile	Lys	Ser	Ile	Arg	Gly	Ser	Asp	Val	Asp	Ala	Ala	Leu		
			280				285					290					
cac	tac	ttg	gcg	cgc	atg	att	gat	gcc	ggg	gaa	gac	cca	cgg	ttt	att	1027	
His	Tyr	Leu	Ala	Arg	Met	Ile	Asp	Ala	Gly	Glu	Asp	Pro	Arg	Phe	Ile		
			295				300				305						
gcc	cgc	cgg	ttg	gtg	gtt	cac	tca	agt	gaa	gac	atc	ggg	atg	gct	gat	1075	
Ala	Arg	Arg	Leu	Val	Val	His	Ser	Ser	Glu	Asp	Ile	Gly	Met	Ala	Asp		
			310			315				320				325			
cct	tcg	gcc	atg	caa	gtg	gcc	att	gct	gca	gct	caa	gct	gtc	caa	tta	1123	
Pro	Ser	Ala	Met	Gln	Val	Ala	Ile	Ala	Ala	Ala	Gln	Ala	Val	Gln	Leu		
				330					335					340			

atc ggt atg cca gag gcg cgg atc aat ttg gcg caa gcg acc att cat 1171
 Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala Gln Ala Thr Ile His
 345 350 355
 ttg gct ctt gct ccc aaa tcc aat gct gtc atc atg gcc atg gat gct 1219
 Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile Met Ala Met Asp Ala
 360 365 370
 gct ttg act gat gtt cag caa ggc cac atc ggt acc gtt cct gcg cat 1267
 Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly Thr Val Pro Ala His
 375 380 385
 ctt cgc gat ggt cac tat gaa ggc gcc aaa aag ctc gga aat gca gtg 1315
 Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys Leu Gly Asn Ala Val
 390 395 400 405
 gga tat tcc tat cct cac gat gat ccc agg gga gtg gtc cgg caa gaa 1363
 Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly Val Val Arg Gln Glu
 410 415 420
 tat tta ccg gag aac ctg cgc gat cgg gtc tat tac gag ccc acc aca 1411
 Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr Tyr Glu Pro Thr Thr
 425 430 435
 cac ggt gga gag aag cgg att gcc gag tac att ggc agg ctt cgt cgt 1459
 His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile Gly Arg Leu Arg Arg
 440 445 450
 ata atc cgt gga acc aag tagcccggtg tgctcaacac cta 1500
 Ile Ile Arg Gly Thr Lys
 455

<210> 188

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Ala Gln Asp Ser Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala
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 Gly Asn Thr Ser Ser Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe
 20 25 30
 His Pro Gly Gly His Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr
 35 40 45
 Leu Asp Glu Val Val Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro
 50 55 60
 Leu Arg Arg Leu Ile Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr
 65 70 75 80
 Gly Pro Pro Gly Thr Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala
 85 90 95
 Ala Ala Gly Asp Arg Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val
 100 105 110

Lys Glu Val Arg Ala Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu
 115 120 125
 Gly Gln Arg Thr Val Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys
 130 135 140
 Thr Gln Gln Asp Ala Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu
 145 150 155 160
 Leu Val Ala Ala Thr Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro
 165 170 175
 Leu Leu Ser Arg Ser Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu
 180 185 190
 Asp Ile Lys Thr Val Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu
 195 200 205
 Ala Gly Arg Ile Thr Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu
 210 215 220
 Leu Ala Gly Gly Asp Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala
 225 230 235 240
 Ala Glu Ala Val Glu Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met
 245 250 255
 Ala Asn Val Asn Arg Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln
 260 265 270
 His Tyr Asp Val Val Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp
 275 280 285
 Val Asp Ala Ala Leu His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu
 290 295 300
 Asp Pro Arg Phe Ile Ala Arg Arg Leu Val Val His Ser Ser Glu Asp
 305 310 315 320
 Ile Gly Met Ala Asp Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala
 325 330 335
 Gln Ala Val Gln Leu Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala
 340 345 350
 Gln Ala Thr Ile His Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile
 355 360 365
 Met Ala Met Asp Ala Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly
 370 375 380
 Thr Val Pro Ala His Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys
 385 390 395 400
 Leu Gly Asn Ala Val Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly
 405 410 415
 Val Val Arg Gln Glu Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr
 420 425 430
 Tyr Glu Pro Thr Thr His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile

435

440

445

Gly Arg Leu Arg Arg Ile Ile Arg Gly Thr Lys
 450 455

<210> 189

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA00287

<400> 189

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caggaaaaat tgttgtgagg gtataaagag gacttgaaaa atg cac cat cta cgc 115
 Met His His Leu Arg
 1 5

tat gaa tca cca atc gga gag ctt ctt ctt gtt gca agt gac caa ggg 163
 Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val Ala Ser Asp Gln Gly
 10 15 20

cta acc tat gtg gca ttc tcc gat gaa aac tac gca gct tgt act gtc 211
 Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr Ala Ala Cys Thr Val
 25 30 35

ggg tcg acc ccg gga acc aat gcg gtg ctg gaa cag gca gtt gct gag 259
 Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu Gln Ala Val Ala Glu
 40 45 50

ctt gaa gaa tac ttc gca ggg aaa cgt aaa gag ttc agc act ccc ctg 307
 Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu Phe Ser Thr Pro Leu
 55 60 65

gat tgg cca agc caa aat ctg ctg agc ttc cgc ggt aaa gtg cag gaa 355
 Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg Gly Lys Val Gln Glu
 70 75 80 85

ttt ttg ctg tcc att cct tat ggg gag agt aaa act tac aaa cag atc 403
 Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys Thr Tyr Lys Gln Ile
 90 95 100

gcc gct gag ctt aat aat gtg ggc gcg gtt cgt gca gtg gga agc gcc 451
 Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg Ala Val Gly Ser Ala
 105 110 115

tgc gcc acc aac ccc ttg cca atc ttt gct cct tgt cac cga gta ctg 499
 Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro Cys His Arg Val Leu
 120 125 130

cgc act gat ggg gcg tta ggt ggc tac aga gga ggc ttg gaa gca aaa 547
 Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly Gly Leu Glu Ala Lys
 135 140 145

cag tgg ctg ttg gag ctg gaa cgt cct tagttttgtgt ccgcgcacgg agc 597
 Gln Trp Leu Leu Glu Leu Glu Arg Pro

155

<400> 190															
Met	His	His	Leu	Arg	Tyr	Glu	Ser	Pro	Ile	Gly	Glu	Leu	Leu	Leu	Val
1				5					10					15	
Ala	Ser	Asp	Gln	Gly	Leu	Thr	Tyr	Val	Ala	Phe	Ser	Asp	Glu	Asn	Tyr
			20					25					30		
Ala	Ala	Cys	Thr	Val	Gly	Ser	Thr	Pro	Gly	Thr	Asn	Ala	Val	Leu	Glu
		35					40					45			
Gln	Ala	Val	Ala	Glu	Leu	Glu	Glu	Tyr	Phe	Ala	Gly	Lys	Arg	Lys	Glu
	50					55					60				
Phe	Ser	Thr	Pro	Leu	Asp	Trp	Pro	Ser	Gln	Asn	Leu	Leu	Ser	Phe	Arg
65					70					75					80
Gly	Lys	Val	Gln	Glu	Phe	Leu	Leu	Ser	Ile	Pro	Tyr	Gly	Glu	Ser	Lys
				85					90					95	
Thr	Tyr	Lys	Gln	Ile	Ala	Ala	Glu	Leu	Asn	Asn	Val	Gly	Ala	Val	Arg
			100					105					110		
Ala	Val	Gly	Ser	Ala	Cys	Ala	Thr	Asn	Pro	Leu	Pro	Ile	Phe	Ala	Pro
		115					120					125			
Cys	His	Arg	Val	Leu	Arg	Thr	Asp	Gly	Ala	Leu	Gly	Gly	Tyr	Arg	Gly
	130					135					140				
Gly	Leu	Glu	Ala	Lys	Gln	Trp	Leu	Leu	Glu	Leu	Glu	Arg	Pro		
145					150						155				

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<400> 191
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gaatctaaac tattcccaaa tagaccatac ggtctaacat gtg ttc atg ctt gca 115
                                         Val Phe Met Leu Ala
                                         1                               5

cag cga aca ctc ccc att cac atc acc gcc ccc cac cta ccc gtc gcg 163
Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro His Leu Pro Val Ala
                        10                        15                        20

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cgc gta ttt cat caa att cgc gcc aca gac gcc gat cgc acc tct ctg	211
Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala Asp Arg Thr Ser Leu	
25 30 35	
caa cgc gat ctt gaa ctc tcc caa gct ggc atc acg cgg cat gtg tca	259
Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile Thr Arg His Val Ser	
40 45 50	
gcg ctt att gat gca ggt ctc gtg gag gaa acc cga gtg gat tcc ggg	307
Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr Arg Val Asp Ser Gly	
55 60 65	
gcg cgc tcg ggg cga ccg cgc aca aaa tta ggc atc gac ggc cgc cat	355
Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly Ile Asp Gly Arg His	
70 75 80 85	
ctc acc gcc tgg gga gtg cac att ggc ctg cgc agc acg gat ttt gcg	403
Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg Ser Thr Asp Phe Ala	
90 95 100	
gtg tgc gat tta gcc ggc cga gtg att agg tat gag cgc gtg gac cat	451
Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr Glu Arg Val Asp His	
105 110 115	
gaa gtt tca cac tcc acg ccg tcg gaa acg ctg aat ttt gtc gca cat	499
Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu Asn Phe Val Ala His	
120 125 130	
agg tta caa aca ttg agc gcc ggc ttg ccc gag ccc cgc aat gtg ggc	547
Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu Pro Arg Asn Val Gly	
135 140 145	
gtg gca tta tct gcc cac tta agc gcc aac gga acc gtc act tcc gaa	595
Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly Thr Val Thr Ser Glu	
150 155 160 165	
gat tat ggc tgg tca gag gtg gaa att ggg gca cac ctc ccc ttc ccc	643
Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala His Leu Pro Phe Pro	
170 175 180	
gcc acc atc gga tca ggt gtt gcg gcg atg gcc ggt tcg gaa att atc	691
Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala Gly Ser Glu Ile Ile	
185 190 195	
aac gcg cca ctg acc caa tcc acg cag tcc acg ctg tat ttc tac gcc	739
Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr Leu Tyr Phe Tyr Ala	
200 205 210	
cgc gaa atg gtc tcc cac gcc tgg att ttc aac ggc gct gtc cac cgc	787
Arg Glu Met Val Ser His Ala Trp Ile Phe Asn Gly Ala Val His Arg	
215 220 225	
ccc aac agc ggc cgc acg ccg acg gcg ttc gga aat aca aat acc tta	835
Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly Asn Thr Asn Thr Leu	
230 235 240 245	
aaa gat gct ttt cga cgt gga ctc aca cca aca act ttc tcc gat tta	883
Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr Thr Phe Ser Asp Leu	
250 255 260	

gtc caa ctc tcc cac acc aac ccg ctt gca cga cag atc ctc aac gag 931
 Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg Gln Ile Leu Asn Glu
 265 270 275

cgc gcc cac aaa ctt gcc gac gcc gta acc acc gcc gtt gat gtt gtc 979
 Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr Ala Val Asp Val Val
 280 285 290

gac ccc gaa gcc gtc gtc ttc gcc ggc gaa gcc ttc acc ctg gat ccg 1027
 Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala Phe Thr Leu Asp Pro
 295 300 305

gaa act ctt cgc att gtg gtg acc cag ctc cga gca aac acc ggc agc 1075
 Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg Ala Asn Thr Gly Ser
 310 315 320 325

caa ctg aga atc caa cgc gca gac gcc tac att ctc cgc acc gcg gcc 1123
 Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile Leu Arg Thr Ala Ala
 330 335 340

atc cag gtg gcg ctg cat ccg atc cgt caa gat ccg ttg gca ttt gtg 1171
 Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp Pro Leu Ala Phe Val
 345 350 355

taattaccac ccatgttgcg ggg 1194

<210> 192

<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Val Phe Met Leu Ala Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro
 1 5 10 15

His Leu Pro Val Ala Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala
 20 25 30

Asp Arg Thr Ser Leu Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile
 35 40 45

Thr Arg His Val Ser Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr
 50 55 60

Arg Val Asp Ser Gly Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly
 65 70 75 80

Ile Asp Gly Arg His Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg
 85 90 95

Ser Thr Asp Phe Ala Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr
 100 105 110

Glu Arg Val Asp His Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu
 115 120 125

Asn Phe Val Ala His Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu
 130 135 140

Pro Arg Asn Val Gly Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly

145	150								155								160	
Thr	Val	Thr	Ser	Glu	Asp	Tyr	Gly	Trp	Ser	Glu	Val	Glu	Ile	Gly	Ala			
				165					170					175				
His	Leu	Pro	Phe	Pro	Ala	Thr	Ile	Gly	Ser	Gly	Val	Ala	Ala	Met	Ala			
				180					185					190				
Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr			
				195					200					205				
Leu	Tyr	Phe	Tyr	Ala	Arg	Glu	Met	Val	Ser	His	Ala	Trp	Ile	Phe	Asn			
				210					215					220				
Gly	Ala	Val	His	Arg	Pro	Asn	Ser	Gly	Arg	Thr	Pro	Thr	Ala	Phe	Gly			
				225					230					235				
Asn	Thr	Asn	Thr	Leu	Lys	Asp	Ala	Phe	Arg	Arg	Gly	Leu	Thr	Pro	Thr			
				245					250					255				
Thr	Phe	Ser	Asp	Leu	Val	Gln	Leu	Ser	His	Thr	Asn	Pro	Leu	Ala	Arg			
				260					265					270				
Gln	Ile	Leu	Asn	Glu	Arg	Ala	His	Lys	Leu	Ala	Asp	Ala	Val	Thr	Thr			
				275					280					285				
Ala	Val	Asp	Val	Val	Asp	Pro	Glu	Ala	Val	Val	Phe	Ala	Gly	Glu	Ala			
				290					295					300				
Phe	Thr	Leu	Asp	Pro	Glu	Thr	Leu	Arg	Ile	Val	Val	Thr	Gln	Leu	Arg			
				305					310					315				
Ala	Asn	Thr	Gly	Ser	Gln	Leu	Arg	Ile	Gln	Arg	Ala	Asp	Ala	Tyr	Ile			
				325					330					335				
Leu	Arg	Thr	Ala	Ala	Ile	Gln	Val	Ala	Leu	His	Pro	Ile	Arg	Gln	Asp			
				340					345					350				
Pro	Leu	Ala	Phe	Val														
				355														

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<210> 193
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01935
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<400> 193
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gcggtctaga taacaagacc cctattagac agcgttgtct atg att ggc tat ggt 115
                                     Met Ile Gly Tyr Gly
                                     1                               5

tta cct atg ccc aat cag gcc cac ttc tct gcg tcc ttt gcc cgc ccc 163
Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala Ser Phe Ala Arg Pro

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10										15					20					
tct	acc	ccg	gct	gca	aag	tgc	atg	cac	cat	atc	cgc	ctc	ggc	cag	caa	211				
Ser	Thr	Pro	Ala	Ala	Lys	Cys	Met	His	His	Ile	Arg	Leu	Gly	Gln	Gln					
			25					30					35							
ctc	att	aga	aat	gag	ctg	gtc	gag	gcc	aca	ggg	ctg	tcc	caa	ccg	act	259				
Leu	Ile	Arg	Asn	Glu	Leu	Val	Glu	Ala	Thr	Gly	Leu	Ser	Gln	Pro	Thr					
		40					45					50								
gtc	acc	cgc	gca	gtc	acc	gct	tta	atg	cag	gca	ggg	ttg	gtt	cgt	gaa	307				
Val	Thr	Arg	Ala	Val	Thr	Ala	Leu	Met	Gln	Ala	Gly	Leu	Val	Arg	Glu					
	55					60					65									
cgc	cct	gat	ctc	aca	ctc	tca	tgc	ggc	cct	ggg	cgt	ccc	aat	att	cct	355				
Arg	Pro	Asp	Leu	Thr	Leu	Ser	Ser	Gly	Pro	Gly	Arg	Pro	Asn	Ile	Pro					
70					75					80					85					
cta	gaa	ctc	gct	cca	agt	cca	tgg	att	cat	gca	ggc	gtg	gca	atc	ggc	403				
Leu	Glu	Leu	Ala	Pro	Ser	Pro	Trp	Ile	His	Ala	Gly	Val	Ala	Ile	Gly					
				90					95					100						
acc	aag	tct	tcc	tac	gtc	gct	ttg	ttt	gat	acc	aag	ggg	cgc	acc	ctt	451				
Thr	Lys	Ser	Ser	Tyr	Val	Ala	Leu	Phe	Asp	Thr	Lys	Gly	Arg	Thr	Leu					
			105					110					115							
cgt	gat	gcc	atg	ctg	gaa	atc	tca	gca	gct	gat	tta	gat	cca	gac	act	499				
Arg	Asp	Ala	Met	Leu	Glu	Ile	Ser	Ala	Ala	Asp	Leu	Asp	Pro	Asp	Thr					
		120					125					130								
ttc	atc	gaa	cac	ctc	att	gct	ggg	gtc	aac	cgc	ctc	acc	act	ggg	ctt	547				
Phe	Ile	Glu	His	Leu	Ile	Ala	Gly	Val	Asn	Arg	Leu	Thr	Thr	Gly	Leu					
	135					140					145									
gat	cta	cca	ctg	gta	ggg	att	ggg	gtt	gcc	acc	tca	gga	aaa	gtc	acc	595				
Asp	Leu	Pro	Leu	Val	Gly	Ile	Gly	Val	Ala	Thr	Ser	Gly	Lys	Val	Thr					
150					155				160					165						
aac	gca	ggc	gtt	gtc	acc	gca	agc	aac	ttg	ggc	tgg	gat	ggc	gtt	gat	643				
Asn	Ala	Gly	Val	Val	Thr	Ala	Ser	Asn	Leu	Gly	Trp	Asp	Gly	Val	Asp					
				170				175						180						
atc	gct	ggc	cgc	ctg	aac	tac	caa	ttc	agc	gtt	cca	gca	acc	gtg	gca	691				
Ile	Ala	Gly	Arg	Leu	Asn	Tyr	Gln	Phe	Ser	Val	Pro	Ala	Thr	Val	Ala					
			185				190						195							
tca	gca	att	cct	gcc	atc	gca	gct	tct	gaa	ctg	cag	gct	tcc	cca	ctt	739				
Ser	Ala	Ile	Pro	Ala	Ile	Ala	Ala	Ser	Glu	Leu	Gln	Ala	Ser	Pro	Leu					
		200				205						210								
ccc	cac	cct	gag	cag	cca	act	ccc	atc	acc	ttg	acc	ttc	tac	gcc	gat	787				
Pro	His	Pro	Glu	Gln	Pro	Thr	Pro	Ile	Thr	Leu	Thr	Phe	Tyr	Ala	Asp					
	215					220					225									
gac	tct	gtg	ggc	gcg	gcc	tac	agc	aat	gat	ttg	gga	gta	cat	gtc	att	835				
Asp	Ser	Val	Gly	Ala	Ala	Tyr	Ser	Asn	Asp	Leu	Gly	Val	His	Val	Ile					
230					235				240					245						
gga	cca	ctg	gct	aca	act	cgt	gga	tca	ggg	ttg	gat	act	ttg	ggc	atg	883				
Gly	Pro	Leu	Ala	Thr	Thr	Arg	Gly	Ser	Gly	Leu	Asp	Thr	Leu	Gly	Met					
				250				255						260						

gct gcc gaa gat gcg ctg agc acc caa ggt ttc tta agc agg gtt tct 931
 Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe Leu Ser Arg Val Ser
 265 270 275
 gat cag ggt atc ttt gcc aac agc ctt ggt gag cta gtc acc att gct 979
 Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu Leu Val Thr Ile Ala
 280 285 290
 aaa gac aat gaa acc gca cgg gaa ttc ctc aac gat cgc gcg acc ctg 1027
 Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn Asp Arg Ala Thr Leu
 295 300 305
 ctg gct cac act gcc gca gaa gct gcc gaa aca gtt aag cca tcc acc 1075
 Leu Ala His Thr Ala Ala Glu Ala Glu Thr Val Lys Pro Ser Thr
 310 315 320 325
 ctg gtt ctc tcg gga tcg gcg ttt tcc gaa gat cca caa ggt cgg tcg 1123
 Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp Pro Gln Gly Arg Ser
 330 335 340
 gtg ttc gct tcc caa ttg aag aag gaa tac gac gca gac att gag ctc 1171
 Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp Ala Asp Ile Glu Leu
 345 350 355
 cgg ttg atc ccc acc cac cgg gaa aac gtc cgc gca gca gct cga gca 1219
 Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg Ala Ala Ala Arg Ala
 360 365 370
 gtc gca ctt gat cga ctg ctc aac gag cca ctt act ctc gta ccc 1264
 Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu Thr Leu Val Pro
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 taacctcatc taagctcagt gct 1287

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 <213> Corynebacterium glutamicum

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 Ser Phe Ala Arg Pro Ser Thr Pro Ala Ala Lys Cys Met His His Ile
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 35 40 45
 Leu Ser Gln Pro Thr Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala
 50 55 60
 Gly Leu Val Arg Glu Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly
 65 70 75 80
 Arg Pro Asn Ile Pro Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala
 85 90 95
 Gly Val Ala Ile Gly Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr

100					105					110					
Lys	Gly	Arg	Thr	Leu	Arg	Asp	Ala	Met	Leu	Glu	Ile	Ser	Ala	Ala	Asp
		115					120					125			
Leu	Asp	Pro	Asp	Thr	Phe	Ile	Glu	His	Leu	Ile	Ala	Gly	Val	Asn	Arg
	130					135					140				
Leu	Thr	Thr	Gly	Leu	Asp	Leu	Pro	Leu	Val	Gly	Ile	Gly	Val	Ala	Thr
	145					150					155				160
Ser	Gly	Lys	Val	Thr	Asn	Ala	Gly	Val	Val	Thr	Ala	Ser	Asn	Leu	Gly
			165						170					175	
Trp	Asp	Gly	Val	Asp	Ile	Ala	Gly	Arg	Leu	Asn	Tyr	Gln	Phe	Ser	Val
			180					185					190		
Pro	Ala	Thr	Val	Ala	Ser	Ala	Ile	Pro	Ala	Ile	Ala	Ala	Ser	Glu	Leu
		195					200					205			
Gln	Ala	Ser	Pro	Leu	Pro	His	Pro	Glu	Gln	Pro	Thr	Pro	Ile	Thr	Leu
	210					215					220				
Thr	Phe	Tyr	Ala	Asp	Asp	Ser	Val	Gly	Ala	Ala	Tyr	Ser	Asn	Asp	Leu
	225					230					235				240
Gly	Val	His	Val	Ile	Gly	Pro	Leu	Ala	Thr	Thr	Arg	Gly	Ser	Gly	Leu
			245						250					255	
Asp	Thr	Leu	Gly	Met	Ala	Ala	Glu	Asp	Ala	Leu	Ser	Thr	Gln	Gly	Phe
			260					265					270		
Leu	Ser	Arg	Val	Ser	Asp	Gln	Gly	Ile	Phe	Ala	Asn	Ser	Leu	Gly	Glu
		275					280					285			
Leu	Val	Thr	Ile	Ala	Lys	Asp	Asn	Glu	Thr	Ala	Arg	Glu	Phe	Leu	Asn
	290					295					300				
Asp	Arg	Ala	Thr	Leu	Leu	Ala	His	Thr	Ala	Ala	Glu	Ala	Ala	Glu	Thr
	305					310					315				320
Val	Lys	Pro	Ser	Thr	Leu	Val	Leu	Ser	Gly	Ser	Ala	Phe	Ser	Glu	Asp
				325					330					335	
Pro	Gln	Gly	Arg	Ser	Val	Phe	Ala	Ser	Gln	Leu	Lys	Lys	Glu	Tyr	Asp
			340					345					350		
Ala	Asp	Ile	Glu	Leu	Arg	Leu	Ile	Pro	Thr	His	Arg	Glu	Asn	Val	Arg
		355					360					365			
Ala	Ala	Ala	Arg	Ala	Val	Ala	Leu	Asp	Arg	Leu	Leu	Asn	Glu	Pro	Leu
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<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> RXN02270

<400> 195

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               Met Asp Gln Ala Arg
               1 5

ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt 163
Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
               10 15 20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca 211
Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala
               25 30 35

ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg 259
Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met
               40 45 50

tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt 307
Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg
               55 60 65

ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg 355
Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro
               70 75 80 85

ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta 403
Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val
               90 95 100

cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc 451
Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu
               105 110 115

aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa 499
Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys
               120 125 130

aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc 547
Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala
               135 140 145

ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg 595
Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala
               150 155 160 165

caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg 643
Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg
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gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc 691
Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala
               185 190 195

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 Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
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<210> 196

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Glu Gln His Gly Phe Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly
 20 25 30

Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
 35 40 45

Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
 50 55 60

Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
 65 70 75 80

Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
 85 90 95

Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
 100 105 110

Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
 115 120 125

Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
 130 135 140

Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
 145 150 155 160

Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
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Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr
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Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
 195 200 205

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<211> 744

<212> DNA

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<220>

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<222> (101)..(721)

<223> FRXA02270

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ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe 10 15 20															163
tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala 25 30 35															211
ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met 40 45 50															259
tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg 55 60 65															307
ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro 70 75 80 85															355
ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val 90 95 100															403
cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tcg ctc atg ctc Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu 105 110 115															451
aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys 120 125 130															499
aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala 135 140 145															547
ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala 150 155 160 165															595
caa cgt caa gga aaa caa gtg tct gtc atc aac ggc ggc cca ggt cgg Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg 170 175 180															643
gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca ccg gcc Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala 185 190 195															691
ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag ttc Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu 200 205															744

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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
 35 40 45
 Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
 50 55 60
 Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
 65 70 75 80
 Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
 85 90 95
 Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
 100 105 110
 Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
 115 120 125
 Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
 130 135 140
 Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
 145 150 155 160
 Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
 165 170 175
 Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr
 180 185 190
 Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
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 <212> DNA
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 <222> (101)..(580)
 <223> RXA01241

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	Val	Asp	Val	Arg	His	
	1				5	
ctt cca gaa act gaa agc cgt tcc tcc aag gct gct aca cag gca aag						163
Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala Ala Thr Gln Ala Lys						
			10		15	20
agc aag gcc cct cag gcc ggg gtc cat gat cct gag tta gct ggc cag						211
Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro Glu Leu Ala Gly Gln			25		30	35
acc tca ttt gtc cca gtg gtg ggc aaa att gcc gct ggt agc ccg atc						259
Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala Ala Gly Ser Pro Ile			40		45	50
acc gct gag cag aac atc gaa gag tac tac cca ctc ccc gca gaa atc						307
Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro Leu Pro Ala Glu Ile			55		60	65
gtc gga gac ggt gac ttg ttc atg ctc cag gtt gtt ggc gag tcc atg						355
Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val Val Gly Glu Ser Met			70		75	80
						85
agg gat gct ggc atc ctc acc ggc gac tgg gtt gtt gtt cgt tcc cag						403
Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val Val Val Arg Ser Gln			90		95	100
ccg gta gct gag cag gcc gag ttc gtc gcg gca atg att gac ggt gaa						451
Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala Met Ile Asp Gly Glu			105		110	115
gcc acc gtg aag gaa ttc cac aag gat tca tct ggc atc tgg ctc ctg						499
Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser Gly Ile Trp Leu Leu			120		125	130
cca cac aac gat acg ttt gcc cca att cct gct gag aat gca gaa atc						547
Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala Glu Asn Ala Glu Ile			135		140	145
atg ggc aag gtt gtt tcc gtg atg cgc aag ctt taagtcgctt ttcaggttcc						600
Met Gly Lys Val Val Ser Val Met Arg Lys Leu			150		155	160
cgc						603

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<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Ala	Thr	Gln	Ala	Lys	Ser	Lys	Ala	Pro	Gln	Ala	Gly	Val	His	Asp	Pro
		20					25						30		

Glu	Leu	Ala	Gly	Gln	Thr	Ser	Phe	Val	Pro	Val	Val	Gly	Lys	Ile	Ala
		35					40					45			

Ala Gly Ser Pro Ile Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro
 50 55 60

Leu Pro Ala Glu Ile Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val
 65 70 75 80

Val Gly Glu Ser Met Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val
 85 90 95

Val Val Arg Ser Gln Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala
 100 105 110

Met Ile Asp Gly Glu Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser
 115 120 125

Gly Ile Trp Leu Leu Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala
 130 135 140

Glu Asn Ala Glu Ile Met Gly Lys Val Val Ser Val Met Arg Lys Leu
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 <211> 777
 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Ser Glu Thr Val
 1 5

tta gtc ata gga gca aca gga agc ata ggc cga cat gtt gtc tcg gaa 163
 Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg His Val Val Ser Glu
 10 15 20

gca ctt aac cag gga tac caa gtt aag gca ttt gtc cgt agc aag tcc 211
 Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe Val Arg Ser Lys Ser
 25 30 35

cgt gca cgg gtg ctt cca gct gag gca gag att atc gta gga gac ctg 259
 Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile Ile Val Gly Asp Leu
 40 45 50

ctt gat cct tcc tcg att gag aaa gct gta aaa ggc gtc gag gga atc 307
 Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys Gly Val Glu Gly Ile
 55 60 65

att ttc act cac ggc acc tcc act cgt aaa agc gat gtg cgg gat gtt 355
 Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser Asp Val Arg Asp Val
 70 75 80 85

gat tac acc ggc gtt gcc aac acg ttg aag gca gtc aag gga aaa gat 403
Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala Val Lys Gly Lys Asp
90 95 100

gta aaa att gtg ctg atg acc gcc gtt gga acg acc cgc cca ggt gtg 451
Val Lys Ile Val Leu Met Thr Ala Val Gly Thr Thr Arg Pro Gly Val
105 110 115

gct tat gcc gag tgg aag cga cat ggc gag caa ctt gtt cga gct agc 499
Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln Leu Val Arg Ala Ser
120 125 130

gga cac ggt tac acc att gtt cgc cct ggt tgg ttt gat tac aac aac 547
Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp Phe Asp Tyr Asn Asn
135 140 145

gat gac gag cgt cag atc gtc atg ctt caa ggc gac acc aat cag tcg 595
Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly Asp Thr Asn Gln Ser
150 155 160 165

ggt ggc cca gcc gat ggc gtg att gcg cgt gat caa atc gcg cga gtt 643
Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp Gln Ile Ala Arg Val
170 175 180

ttg gtt agc agt ttg aat gat gca aaa gca cga aac aaa acc ttc gag 691
Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg Asn Lys Thr Phe Glu
185 190 195

ctt tct gcc act tat gga cct gcc caa gga aag cct gac cgc aac ttt 739
Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys Pro Asp Arg Asn Phe
200 205 210

tgc agc act tcg ggc tgacgatacc gatgatattg acg 777
Cys Ser Thr Ser Gly
215

<210> 202

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Met Ser Glu Thr Val Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg
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His Val Val Ser Glu Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe
20 25 30

Val Arg Ser Lys Ser Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile
35 40 45

Ile Val Gly Asp Leu Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys
50 55 60

Gly Val Glu Gly Ile Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser
65 70 75 80

Asp Val Arg Asp Val Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala
85 90 95

Val Lys Gly Lys Asp Val Lys Ile Val Leu Met Thr Ala Val Gly Thr
 100 105 110

Thr Arg Pro Gly Val Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln
 115 120 125

Leu Val Arg Ala Ser Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp
 130 135 140

Phe Asp Tyr Asn Asn Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly
 145 150 155 160

Asp Thr Asn Gln Ser Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp
 165 170 175

Gln Ile Ala Arg Val Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg
 180 185 190

Asn Lys Thr Phe Glu Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys
 195 200 205

Pro Asp Arg Asn Phe Cys Ser Thr Ser Gly
 210 215

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 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(838)
 <223> RXA00583

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 Val Tyr Glu Arg Arg
 1 5

ctt tta aga gaa cta gac ggc gcc aaa cag ccc ggt cac gtt gcc atc 163
 Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro Gly His Val Ala Ile
 10 15 20

atg tgt gat ggc aac cga cgc tgg gcc cgg gaa gcg ggc ttc act gat 211
 Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu Ala Gly Phe Thr Asp
 25 30 35

gtc agc cat ggg cac cga gtg ggt gcc aaa aag atc ggc gag atg gtc 259
 Val Ser His Gly His Arg Val Gly Ala Lys Lys Ile Gly Glu Met Val
 40 45 50

cgc tgg tgt gat gat gta gac gtc aat ctc gtg acc gtt tat ttg ctg 307
 Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val Thr Val Tyr Leu Leu
 55 60 65

tct atg gaa aac ctt ggg cga tcc tcc gaa gag ctg caa ttg ctg ttc 355
 Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu Leu Gln Leu Leu Phe

70	75	80	85	
gat atc atc gcc gat gtc gct gat gaa ctc gcg cgt cct gaa acc aac				403
Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala Arg Pro Glu Thr Asn	90	95	100	
tgt cga gtc cgc ctc gtt ggt cat tta gat ctg ctc cca gac cca gtt				451
Cys Arg Val Arg Leu Val Gly His Leu Asp Leu Leu Pro Asp Pro Val	105	110	115	
gct tgt cgt tta cgc aaa gct gaa gaa gct acc gtt aac aac aca ggc				499
Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr Val Asn Asn Thr Gly	120	125	130	
atc gca gtc aac atg gct gtc ggt tat ggc gga cgc cag gaa atc gtt				547
Ile Ala Val Asn Met Ala Val Gly Tyr Gly Arg Gln Glu Ile Val	135	140	145	
gat gcc gtg caa aaa ctt ctg acc atc ggc aag gac gag ggc cta agc				595
Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys Asp Glu Gly Leu Ser	150	155	160	165
gtt gat gaa ctg atc gaa tcc gtc aag gta gat gcg atc tcc act cac				643
Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp Ala Ile Ser Thr His	170	175	180	
ctg tac acc tct ggc caa cca gac cca gac ctg gtg atc cgc acc tct				691
Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu Val Ile Arg Thr Ser	185	190	195	
ggt gag cag cga ctt tcc gga ttc atg ctg tgg caa tct gcc tac tcc				739
Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp Gln Ser Ala Tyr Ser	200	205	210	
gaa atc tgg ttc aca gac acc tac tgg cca gcc ttc cga cgc atc gac				787
Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala Phe Arg Arg Ile Asp	215	220	225	
ttc ctc cgc gcc att cgc gac tac tcg cag cgc agc aga aga ttc ggt				835
Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg Ser Arg Arg Phe Gly	230	235	240	245
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Lys				

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<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Val Tyr Glu Arg Arg Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro
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Gly His Val Ala Ile Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu
20 25 30

Ala Gly Phe Thr Asp Val Ser His Gly His Arg Val Gly Ala Lys Lys
35 40 45

Ile Gly Glu Met Val Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val
 50 55 60
 Thr Val Tyr Leu Leu Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu
 65 70 75 80
 Leu Gln Leu Leu Phe Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala
 85 90 95
 Arg Pro Glu Thr Asn Cys Arg Val Arg Leu Val Gly His Leu Asp Leu
 100 105 110
 Leu Pro Asp Pro Val Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr
 115 120 125
 Val Asn Asn Thr Gly Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly
 130 135 140
 Arg Gln Glu Ile Val Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys
 145 150 155 160
 Asp Glu Gly Leu Ser Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp
 165 170 175
 Ala Ile Ser Thr His Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu
 180 185 190
 Val Ile Arg Thr Ser Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp
 195 200 205
 Gln Ser Ala Tyr Ser Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala
 210 215 220
 Phe Arg Arg Ile Asp Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg
 225 230 235 240
 Ser Arg Arg Phe Gly Lys
 245

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(559)
 <223> RXA00592

<400> 205
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 acctcgttgc ttacatgaag cgtgaggtgg cttagttcctt atg gct tct aat tcc 115
 Met Ala Ser Asn Ser
 1 5
 gaa cgc ctt gca gag ctg ggc att tct ctt cct tcc gtt gca gcg cct 163
 Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro Ser Val Ala Ala Pro
 10 15 20

gtt gct gcg tat gtt cct gcg att cag acc ggt aac cag gtg tgg act 211
 Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly Asn Gln Val Trp Thr
 25 30 35

tct ggt cag ctg cct ttc gtt gat ggt cag ctt ccg gcc acc ggc aag 259
 Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu Pro Ala Thr Gly Lys
 40 45 50

gtt ggc gct gag gtt tcc gct gag gat gcg gag aag ttg gct cgt gcg 307
 Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu Lys Leu Ala Arg Ala
 55 60 65

gct gcg cta aac gct ctt gct gcg att gat gcg ctt gtt ggc att gat 355
 Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala Leu Val Gly Ile Asp
 70 75 80 85

aag gtc act cgc gtt ttg aag att gtt ggt ttc gtg gcg tct gct gat 403
 Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe Val Ala Ser Ala Asp
 90 95 100

gat ttc agt ggt cag cct gct gtc gtc aac ggt gct tcc aat ttg atg 451
 Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly Ala Ser Asn Leu Met
 105 110 115

ggt gag gtt ttc ggc gag gct ggg gcg cat gcg cgt tct gct gtg ggc 499
 Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala Arg Ser Ala Val Gly
 120 125 130

gtg gcg gag ttg ccg ctc aac tcg cct gtc gag gtc gag gtt atc gtc 547
 Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu Val Glu Val Ile Val
 135 140 145

gag atc gcg cag tagcacgctt ttcgacgcaa aat 582
 Glu Ile Ala Gln
 150

<210> 206

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

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Ser Val Ala Ala Pro Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly
 20 25 30

Asn Gln Val Trp Thr Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu
 35 40 45

Pro Ala Thr Gly Lys Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu
 50 55 60

Lys Leu Ala Arg Ala Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala
 65 70 75 80

Leu Val Gly Ile Asp Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe
 85 90 95

Val Ala Ser Ala Asp Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly
 100 105 110

Ala Ser Asn Leu Met Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala
 115 120 125

Arg Ser Ala Val Gly Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu
 130 135 140

Val Glu Val Ile Val Glu Ile Ala Gln
 145 150

<210> 207
 <211> 182
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(159)
 <223> RXA00630

<400> 207
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 Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
 1 5 10 15

aac gtc gtg gaa tcc tac atc tcc tac ctg cgc cgc aag gtg gac acc 96
 Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
 20 25 30

cag gat ccg cag cta att cag act gtt cgt ggc gtt gga tat gtt ctg 144
 Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
 35 40 45

cgc acc cca cgt agc taaattctcc tatggaaaat cct 182
 Arg Thr Pro Arg Ser
 50

<210> 208
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
 Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
 1 5 10 15

Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
 20 25 30

Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
 35 40 45

Arg Thr Pro Arg Ser
 50

<210> 209
 <211> 484
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(484)
 <223> FRXA00638

<400> 209
 aatttcaact ctttcagtagc attcacagtt agtattcagtt ggtgttgaag ttccaggggtg 60
 ttccactagtg ggaagttaat cattccgcta atggacacca atg gaa gag ata aaa 115
 Met Glu Glu Ile Lys
 1 5
 atg gac aac cag tct gac gga caa atc cgc gta ctc gtc gtt gat gac 163
 Met Asp Asn Gln Ser Asp Gly Gln Ile Arg Val Leu Val Val Asp Asp
 10 15 20
 gag cca aac atc gtc gag ctg ctc acc gta agc ctt aaa ttc caa ggc 211
 Glu Pro Asn Ile Val Glu Leu Leu Thr Val Ser Leu Lys Phe Gln Gly
 25 30 35
 ttc gca gtg atg acc gcc aac gat ggc aat gaa gcc ctg aag att gct 259
 Phe Ala Val Met Thr Ala Asn Asp Gly Asn Glu Ala Leu Lys Ile Ala
 40 45 50
 cgt gag ttc cgt cca gac gca tac atc ctc gat gtc atg atg cca gga 307
 Arg Glu Phe Arg Pro Asp Ala Tyr Ile Leu Asp Val Met Met Pro Gly
 55 60 65
 atg gac ggc ttc gag ctg ctg acc aag ctg cgc ggc gaa ggc ctt gac 355
 Met Asp Gly Phe Glu Leu Leu Thr Lys Leu Arg Gly Glu Gly Leu Asp
 70 75 80 85
 agc cca gtt ctg tac ctc acc gca aag gat gcc gtg gag cac cgc atc 403
 Ser Pro Val Leu Tyr Leu Thr Ala Lys Asp Ala Val Glu His Arg Ile
 90 95 100
 cac ggc ctg acc atc ggc gct gac gac tac gtg acc aag cct ttc tcc 451
 His Gly Leu Thr Ile Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser
 105 110 115
 ctg gaa gaa gta atc acc cgc ctg cgc gtg att 484
 Leu Glu Glu Val Ile Thr Arg Leu Arg Val Ile
 120 125

<210> 210
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 210
 Met Glu Glu Ile Lys Met Asp Asn Gln Ser Asp Gly Gln Ile Arg Val
 1 5 10 15
 Leu Val Val Asp Asp Glu Pro Asn Ile Val Glu Leu Leu Thr Val Ser
 20 25 30

<400> 211																
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aactagtcgt aattagtcgg attttaagga ggctcacgcc																115
Met Gly Ile Glu Phe																
1 5																
aag	cgt	tca	ccg	cga	ccc	acc	ctg	ggc	gtt	gag	tgg	gaa	att	gca	ctt	163
Lys	Arg	Ser	Pro	Arg	Pro	Thr	Leu	Gly	Val	Glu	Trp	Glu	Ile	Ala	Leu	
10 15 20																
gtt	gat	cca	gaa	aca	cgt	gat	cta	gcc	ccg	cgc	gct	gca	gaa	ata	cta	211
Val	Asp	Pro	Glu	Thr	Arg	Asp	Leu	Ala	Pro	Arg	Ala	Ala	Glu	Ile	Leu	
25 30 35																
gag	att	gtg	gcc	aag	aac	cac	cct	gag	gtg	cac	ctc	gag	cgc	gaa	ttc	259
Glu	Ile	Val	Ala	Lys	Asn	His	Pro	Glu	Val	His	Leu	Glu	Arg	Glu	Phe	
40 45 50																
ctc	caa	aac	acc	gtg	gag	ctt	gtc	acc	gga	gtg	tgc	gac	acc	gtc	ccc	307
Leu	Gln	Asn	Thr	Val	Glu	Leu	Val	Thr	Gly	Val	Cys	Asp	Thr	Val	Pro	
55 60 65																
gaa	gcg	gtg	gca	gag	ctt	tcc	cac	gat	cta	gat	gcg	ctg	aaa	gaa	gca	355
Glu	Ala	Val	Ala	Glu	Leu	Ser	His	Asp	Leu	Asp	Ala	Leu	Lys	Glu	Ala	
70 75 80 85																
gcg	gat	tct	ctc	ggg	ctt	cgg	ttg	tgg	acc	tct	gga	tcc	cac	cca	ttt	403

Ala	Asp	Ser	Leu	Gly	Leu	Arg	Leu	Trp	Thr	Ser	Gly	Ser	His	Pro	Phe	
				90					95					100		
tcg	gat	ttc	cgc	gaa	aac	cca	gta	tct	gaa	aaa	ggc	tcc	tac	gac	gag	451
Ser	Asp	Phe	Arg	Glu	Asn	Pro	Val	Ser	Glu	Lys	Gly	Ser	Tyr	Asp	Glu	
			105					110					115			
atc	atc	gcg	cgc	acc	caa	tac	tgg	gga	aac	cag	atg	ttg	att	tgg	ggc	499
Ile	Ile	Ala	Arg	Thr	Gln	Tyr	Trp	Gly	Asn	Gln	Met	Leu	Ile	Trp	Gly	
		120					125					130				
att	cac	gtc	cac	gtg	ggc	atc	agc	cat	gaa	gat	cgc	gtg	tgg	ccg	atc	547
Ile	His	Val	His	Val	Gly	Ile	Ser	His	Glu	Asp	Arg	Val	Trp	Pro	Ile	
	135					140					145					
atc	aat	gcg	ctg	ctg	aca	aat	tac	cca	cat	ctg	ttg	gca	ctt	tct	gca	595
Ile	Asn	Ala	Leu	Leu	Thr	Asn	Tyr	Pro	His	Leu	Leu	Ala	Leu	Ser	Ala	
150					155					160					165	
agc	tct	cca	gca	tgg	gac	gga	ctt	gat	acc	ggt	tat	gcc	tcc	aac	cgg	643
Ser	Ser	Pro	Ala	Trp	Asp	Gly	Leu	Asp	Thr	Gly	Tyr	Ala	Ser	Asn	Arg	
			170						175					180		
acg	atg	ctc	tac	caa	cag	ctg	cct	aca	gcc	gga	ctg	cca	tac	caa	ttc	691
Thr	Met	Leu	Tyr	Gln	Gln	Leu	Pro	Thr	Ala	Gly	Leu	Pro	Tyr	Gln	Phe	
		185						190					195			
caa	agc	tgg	gat	gaa	tgg	tgc	agc	tac	atg	gcg	gat	caa	gat	aaa	tcc	739
Gln	Ser	Trp	Asp	Glu	Trp	Cys	Ser	Tyr	Met	Ala	Asp	Gln	Asp	Lys	Ser	
		200					205					210				
ggt	gtc	atc	aac	cac	acc	gga	tcc	atg	cac	ttt	gat	atc	cgc	ccc	gca	787
Gly	Val	Ile	Asn	His	Thr	Gly	Ser	Met	His	Phe	Asp	Ile	Arg	Pro	Ala	
	215					220					225					
tcc	aaa	tgg	gga	acc	atc	gaa	gtc	cgc	gtg	gcc	gat	tct	acc	tcc	aac	835
Ser	Lys	Trp	Gly	Thr	Ile	Glu	Val	Arg	Val	Ala	Asp	Ser	Thr	Ser	Asn	
230					235					240					245	
ctg	cgg	gaa	ctg	tct	gcc	atc	gtg	gcg	ttg	acc	cac	tgt	ctc	gtg	gtg	883
Leu	Arg	Glu	Leu	Ser	Ala	Ile	Val	Ala	Leu	Thr	His	Cys	Leu	Val	Val	
			250					255						260		
cac	tac	gac	cgc	atg	atc	gac	gct	ggc	gaa	gag	ctt	ccc	tcc	ctg	caa	931
His	Tyr	Asp	Arg	Met	Ile	Asp	Ala	Gly	Glu	Glu	Leu	Pro	Ser	Leu	Gln	
		265						270					275			
caa	tgg	cac	gtt	tcg	gaa	aat	aaa	tgg	cgc	gcg	gct	agg	tat	ggt	ctg	979
Gln	Trp	His	Val	Ser	Glu	Asn	Lys	Trp	Arg	Ala	Ala	Arg	Tyr	Gly	Leu	
		280					285					290				
gat	gcc	gaa	atc	atc	att	tcc	aga	gac	acc	gat	gaa	gcg	atg	gtt	caa	1027
Asp	Ala	Glu	Ile	Ile	Ile	Ser	Arg	Asp	Thr	Asp	Glu	Ala	Met	Val	Gln	
	295					300					305					
gac	gaa	ctc	cgc	cga	cta	gta	gcg	caa	ttg	atg	cct	cta	gcc	aac	gaa	1075
Asp	Glu	Leu	Arg	Arg	Leu	Val	Ala	Gln	Leu	Met	Pro	Leu	Ala	Asn	Glu	
310					315					320					325	
ctc	ggc	tgc	gct	cgt	gag	ctt	gaa	ctt	gtg	ttg	gaa	atc	ctg	gaa	cgt	1123
Leu	Gly	Cys	Ala	Arg	Glu	Leu	Glu	Leu	Val	Leu	Glu	Ile	Leu	Glu	Arg	

330										335					340					
ggt	ggt	gga	tac	gaa	cgc	caa	cgc	aga	gtg	ttt	aaa	gaa	act	ggc	agt	1171				
Gly	Gly	Gly	Tyr	Glu	Arg	Gln	Arg	Arg	Val	Phe	Lys	Glu	Thr	Gly	Ser					
			345					350					355							
tgg	aaa	gct	gca	ggt	gat	tta	gcc	tgc	gac	gaa	ctc	aac	gac	ctc	aaa	1219				
Trp	Lys	Ala	Ala	Val	Asp	Leu	Ala	Cys	Asp	Glu	Leu	Asn	Asp	Leu	Lys					
		360					365					370								
gca	ctg	gac	taa	atagcta	tggtggaatc	cca										1251				
Ala	Leu	Asp																		
		375																		

<210> 212
 <211> 376
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 212
 Met Gly Ile Glu Phe Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu
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 Trp Glu Ile Ala Leu Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg
 20 25 30
 Ala Ala Glu Ile Leu Glu Ile Val Ala Lys Asn His Pro Glu Val His
 35 40 45
 Leu Glu Arg Glu Phe Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val
 50 55 60
 Cys Asp Thr Val Pro Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp
 65 70 75 80
 Ala Leu Lys Glu Ala Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser
 85 90 95
 Gly Ser His Pro Phe Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys
 100 105 110
 Gly Ser Tyr Asp Glu Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln
 115 120 125
 Met Leu Ile Trp Gly Ile His Val His Val Gly Ile Ser His Glu Asp
 130 135 140
 Arg Val Trp Pro Ile Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu
 145 150 155 160
 Leu Ala Leu Ser Ala Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly
 165 170 175
 Tyr Ala Ser Asn Arg Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly
 180 185 190
 Leu Pro Tyr Gln Phe Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala
 195 200 205
 Asp Gln Asp Lys Ser Gly Val Ile Asn His Thr Gly Ser Met His Phe

210	215	220
Asp Ile Arg Pro Ala Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala 225 230 235 240		
Asp Ser Thr Ser Asn Leu Arg Glu Leu Ser Ala Ile Val Ala Leu Thr 245 250 255		
His Cys Leu Val Val His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu 260 265 270		
Leu Pro Ser Leu Gln Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala 275 280 285		
Ala Arg Tyr Gly Leu Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp 290 295 300		
Glu Ala Met Val Gln Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met 305 310 315 320		
Pro Leu Ala Asn Glu Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu 325 330 335		
Glu Ile Leu Glu Arg Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe 340 345 350		
Lys Glu Thr Gly Ser Trp Lys Ala Ala Val Asp Leu Ala Cys Asp Glu 355 360 365		
Leu Asn Asp Leu Lys Ala Leu Asp 370 375		

<210> 213
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(664)
 <223> RXA01450

<400> 213
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 gcctcctgat taggttctta cccaacgatt gctaggatat gtg cct gtg acc ctt 115
 Val Pro Val Thr Leu
 1 5
 act ctt gga atc gtc ggc ctg ccc aac gtt ggc aag tcc acc ctg ttc 163
 Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Leu Phe
 10 15 20
 aac gcc ctg act cgc aat gac gtg ctc gca gcg aac tac ccg ttc gcc 211
 Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala Asn Tyr Pro Phe Ala
 25 30 35
 acc atc gag cca aac gtg ggc ctt gtc gag ctt cca gac gct cgc ctt 259
 Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu Pro Asp Ala Arg Leu
 40 45 50

gaa cgc ctt tct gaa atc ttc ggc tct gag cgc atc ctg cca gca acc 307
 Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg Ile Leu Pro Ala Thr
 55 60 65

gtg tct ttc gtt gac atc gcc gga atc gtt aag gga gct tcc gaa ggc 355
 Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys Gly Ala Ser Glu Gly
 70 75 80 85

gaa gga atg ggc aac gct ttc ctt gcc aac atc cgc gaa gca gac gct 403
 Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile Arg Glu Ala Asp Ala
 90 95 100

atc tgt cag gtt gtg cgc gca ttc gct gac gaa aac gtc att cac gtc 451
 Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu Asn Val Ile His Val
 105 110 115

gat ggt gaa gtt aac cca gca acc gat atc tct gtg atc aac acc gag 499
 Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser Val Ile Asn Thr Glu
 120 125 130

ctg atc ctc gcc gac ctg cag acc gtg gaa aaa gca ctc cca cgc ctc 547
 Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys Ala Leu Pro Arg Leu
 135 140 145

gaa aag gat gca cgc aaa gac aag gga ctt ggc gaa gtc gta gat gag 595
 Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly Glu Val Val Asp Glu
 150 155 160 165

acc aaa aaa gcc ctt gcg atc ttg agc gat gac cgc acc ttg ttt ctc 643
 Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp Arg Thr Leu Phe Leu
 170 175 180

tgc agc aaa agc tgg cga cat tgatctggcc ctccctgcgcg atc 687
 Cys Ser Lys Ser Trp Arg His
 185

<210> 214
 <211> 188
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Val Pro Val Thr Leu Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly
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Lys Ser Thr Leu Phe Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala
 20 25 30

Asn Tyr Pro Phe Ala Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu
 35 40 45

Pro Asp Ala Arg Leu Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg
 50 55 60

Ile Leu Pro Ala Thr Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys
 65 70 75 80

Gly Ala Ser Glu Gly Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile
 85 90 95

Arg Glu Ala Asp Ala Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu
 100 105 110
 Asn Val Ile His Val Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser
 115 120 125
 Val Ile Asn Thr Glu Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys
 130 135 140
 Ala Leu Pro Arg Leu Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly
 145 150 155 160
 Glu Val Val Asp Glu Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp
 165 170 175
 Arg Thr Leu Phe Leu Cys Ser Lys Ser Trp Arg His
 180 185

<210> 215
 <211> 690
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(667)
 <223> RXA01451

<400> 215
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 Met Thr Ala Pro Cys
 1 5
 ttc tct gca gca aaa gct ggc gac att gat ctg gcc ctc ctg cgc gat 163
 Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu Ala Leu Leu Arg Asp
 10 15 20
 ctc cac ctg atg aca gca aag cct ttc ctc tac gtc ttc aac tcc gac 211
 Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr Val Phe Asn Ser Asp
 25 30 35
 gaa aaa gtg ctc acc gac gac gcc aag aag gac gaa ctc cgc gca cta 259
 Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp Glu Leu Arg Ala Leu
 40 45 50
 gtc gcg cca gca gac tgc gta ttc ctt gac gca caa act gaa acc gaa 307
 Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala Gln Thr Glu Thr Glu
 55 60 65
 ctt ctt gaa ctc gaa gaa gac gaa gca gca gaa ctc ctc gaa gct gta 355
 Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu Leu Leu Glu Ala Val
 70 75 80 85
 ggc caa acg gaa cca ggc cta cac tcc ctc gca cgt gca gga ttt gaa 403
 Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala Arg Ala Gly Phe Glu
 90 95 100

acc ctc gga cta cag acc tac ctc acc gcg ggt cct aag gaa tca cgc 451
 Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly Pro Lys Glu Ser Arg
 105 110 115

gcc tgg acc atc cac aag ggc gac acc gct cca cag gca gca ggc gtt 499
 Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro Gln Ala Ala Gly Val
 120 125 130

atc cat tct gac ttc gaa cgc ggc ttc atc aag gct gaa atc gtc tcc 547
 Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys Ala Glu Ile Val Ser
 135 140 145

ttc gaa gat ctt gac gct gct ggt tcc atg gcg gaa gcc aag gcc cag 595
 Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala Glu Ala Lys Ala Gln
 150 155 160 165

ggc aaa gtc cgc caa gaa ggt aag gac tac gtg atg gtc gat ggc gac 643
 Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val Met Val Asp Gly Asp
 170 175 180

gtt gtg gag ttc cgg ttt aac gtc tagcggttatt gacgctcctc gtt 690
 Val Val Glu Phe Arg Phe Asn Val
 185

<210> 216

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Thr Ala Pro Cys Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu
 1 5 10 15

Ala Leu Leu Arg Asp Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr
 20 25 30

Val Phe Asn Ser Asp Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp
 35 40 45

Glu Leu Arg Ala Leu Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala
 50 55 60

Gln Thr Glu Thr Glu Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu
 65 70 75 80

Leu Leu Glu Ala Val Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala
 85 90 95

Arg Ala Gly Phe Glu Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly
 100 105 110

Pro Lys Glu Ser Arg Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro
 115 120 125

Gln Ala Ala Gly Val Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys
 130 135 140

Ala Glu Ile Val Ser Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala
 145 150 155 160

Glu Ala Lys Ala Gln Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val
 165 170 175

Met Val Asp Gly Asp Val Val Glu Phe Arg Phe Asn Val
 180 185

<210> 217
 <211> 1626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1603)
 <223> RXA02376

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 Met Asn Arg Phe Ile
 1 5
 gac cgc gtt gtg cta cac ctc gcc gca ggt gac ggc ggc aat ggt tgt 163
 Asp Arg Val Val Leu His Leu Ala Ala Gly Asp Gly Gly Asn Gly Cys
 10 15 20
 gtc tcg gtg cac cgc gaa aaa ttc aag cca ctt ggt gga cca gac ggc 211
 Val Ser Val His Arg Glu Lys Phe Lys Pro Leu Gly Gly Pro Asp Gly
 25 30 35
 ggc aac ggc ggc cac ggt gga gac atc atc ttg gaa gtc acc gca cag 259
 Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu Glu Val Thr Ala Gln
 40 45 50
 gtc cac acc ctg ctt gac ttc cac ttc cac cca cac gtg aag gcc gag 307
 Val His Thr Leu Leu Asp Phe His Phe His Pro His Val Lys Ala Glu
 55 60 65
 cgc ggc gct aac ggc gct ggc gat cat cgc aac ggt gcc cga ggc aag 355
 Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn Gly Ala Arg Gly Lys
 70 75 80 85
 gac ctt gtc ttg gaa gtt cca cca gga act gtc gtg ctt aat gaa aag 403
 Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val Val Leu Asn Glu Lys
 90 95 100
 ggc gag act ctg gca gac ctg acc agc gtg ggc atg aag ttc atc gct 451
 Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly Met Lys Phe Ile Ala
 105 110 115
 gct gct ggc ggt aac ggc ggt ttg ggt aac gca gcg ctt gcc tcc aag 499
 Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala Ala Leu Ala Ser Lys
 120 125 130
 gct cgt aag gcc cca ggc ttc gcc ctg atc ggt gag cca ggc gag gcc 547
 Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly Glu Pro Gly Glu Ala
 135 140 145
 cac gac ttg att ctt gaa ctc aaa tcc atg gca gat gtg gga ttg gtg 595

His 150	Asp	Leu	Ile	Leu	Glu 155	Leu	Lys	Ser	Met	Ala 160	Asp	Val	Gly	Leu	Val 165	
ggc	ttc	cca	tca	gcc	ggc	aaa	tca	tca	ctg	att	tct	gtg	atg	tct	gca	643
Gly	Phe	Pro	Ser	Ala 170	Gly	Lys	Ser	Ser	Leu 175	Ile	Ser	Val	Met	Ser 180	Ala	
gca	aag	cca	aag	atc	ggt	gat	tac	cca	ttc	acc	acc	ctg	cag	cca	aac	691
Ala	Lys	Pro	Lys 185	Ile	Gly	Asp	Tyr	Pro	Phe 190	Thr	Thr	Leu	Gln 195	Pro	Asn	
ctc	ggc	gta	gtt	aac	gtt	ggt	cat	gag	act	ttc	acc	atg	gca	gac	gtg	739
Leu	Gly	Val 200	Val	Asn	Val	Gly	His 205	Glu	Thr	Phe	Thr	Met 210	Ala	Asp	Val	
cct	ggt	ttg	atc	cct	ggt	gct	tct	gag	ggc	aag	ggc	ttg	ggt	ctg	gat	787
Pro	Gly 215	Leu	Ile	Pro	Gly	Ala 220	Ser	Glu	Gly	Lys	Gly 225	Leu	Gly	Leu	Asp	
ttc	ttg	cgc	cac	att	gag	cgc	acc	tcc	gtg	ctg	gtt	cac	gtt	gtc	gat	835
Phe	Leu	Arg	His	Ile	Glu 235	Arg	Thr	Ser	Val	Leu 240	Val	His	Val	Val	Asp 245	
acc	gca	acg	atg	gat	cca	ggc	cgc	gat	ccg	atc	tct	gat	att	gag	gct	883
Thr	Ala	Thr	Met 250	Asp	Pro	Gly	Arg	Asp	Pro 255	Ile	Ser	Asp	Ile	Glu 260	Ala	
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Leu	Glu	Ala	Glu 265	Leu	Ala	Ala	Tyr 270	Gln	Ser	Ala	Leu	Asp	Glu 275	Asp	Thr	
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Gly	Leu	Gly 280	Asp	Leu	Ser	Gln 285	Arg	Pro	Arg	Leu	Val 290	Val	Leu	Asn	Lys	
gct	gat	gtc	cct	gag	gct	gaa	gag	ctt	gct	gag	ttc	ctc	aaa	gaa	gat	1027
Ala	Asp	Val 295	Pro	Glu	Ala	Glu 300	Glu	Leu	Ala	Glu	Phe 305	Leu	Lys	Glu	Asp	
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Ile	Glu	Lys	Gln	Phe	Gly 315	Trp	Pro	Val	Phe	Ile 320	Ile	Ser	Ala	Val	Ala 325	
cgc	aag	ggc	ttg	gat	cct	ttg	aag	tac	aag	ctg	ctg	gaa	atc	gtc	cag	1123
Arg	Lys	Gly	Leu 330	Asp	Pro	Leu	Lys	Tyr	Lys 335	Leu	Leu	Glu	Ile	Val 340	Gln	
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Asp	Ala	Arg	Lys 345	Lys	Arg	Pro	Lys	Glu 350	Lys	Ala	Glu	Ser	Val 355	Ile	Ile	
aag	cct	aag	gct	gtt	gat	cac	cgc	act	aag	ggg	cag	ttc	cag	atc	aag	1219
Lys	Pro	Lys 360	Ala	Val	Asp	His	Arg 365	Thr	Lys	Gly	Gln 370	Phe	Gln	Ile	Lys	
cct	gac	cca	gag	gtt	cag	ggc	gga	ttc	atc	atc	acc	ggc	gaa	aag	cca	1267
Pro	Asp	Pro	Glu	Val	Gln	Gly 380	Gly	Phe	Ile	Ile	Thr 385	Gly	Glu	Lys	Pro	
gag	cgc	tgg	att	ttg	cag	acc	gac	ttt	gaa	aac	gac	gaa	gca	gtt	ggc	1315
Glu	Arg	Trp	Ile	Leu	Gln	Thr	Asp	Phe	Glu	Asn	Asp	Glu	Ala	Val	Gly	

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Tyr Leu Ala Asp Arg Leu Ala Lys Leu Gly Ile Glu Asp Gly Leu Arg	410	415	420	
aag gca gga gca cat gtg ggt gca aac gtc acc atc gga ggc att tcc				1411
Lys Ala Gly Ala His Val Gly Ala Asn Val Thr Ile Gly Gly Ile Ser	425	430	435	
ttc gag tgg gag cca atg acc acc gct ggc gac gat cca gtc ctt acc				1459
Phe Glu Trp Glu Pro Met Thr Thr Ala Gly Asp Asp Pro Val Leu Thr	440	445	450	
gga cgt ggc acc gat gtg cgc ctt gaa cag acc tct cgt atc tct gct				1507
Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr Ser Arg Ile Ser Ala	455	460	465	
gca gag cgt aaa cgc gca tct cag gta cgt cgt ggc ctc atc gat gag				1555
Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg Gly Leu Ile Asp Glu	470	475	480	485
ttg gat tat ggc gag gac caa gag gct tcc cgc gaa cgc tgg gaa gga				1603
Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg Glu Arg Trp Glu Gly	490	495	500	
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<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

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Gly Gly Pro Asp Gly Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu	35	40	45	
Glu Val Thr Ala Gln Val His Thr Leu Leu Asp Phe His Phe His Pro	50	55	60	
His Val Lys Ala Glu Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn	65	70	75	80
Gly Ala Arg Gly Lys Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val	85	90	95	
Val Leu Asn Glu Lys Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly	100	105	110	
Met Lys Phe Ile Ala Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala	115	120	125	
Ala Leu Ala Ser Lys Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly	130	135	140	

Glu	Pro	Gly	Glu	Ala	His	Asp	Leu	Ile	Leu	Glu	Leu	Lys	Ser	Met	Ala	
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Asp	Val	Gly	Leu	Val	Gly	Phe	Pro	Ser	Ala	Gly	Lys	Ser	Ser	Leu	Ile	
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Ser	Val	Met	Ser	Ala	Ala	Lys	Pro	Lys	Ile	Gly	Asp	Tyr	Pro	Phe	Thr	
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Thr	Leu	Gln	Pro	Asn	Leu	Gly	Val	Val	Asn	Val	Gly	His	Glu	Thr	Phe	
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Thr	Met	Ala	Asp	Val	Pro	Gly	Leu	Ile	Pro	Gly	Ala	Ser	Glu	Gly	Lys	
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Gly	Leu	Gly	Leu	Asp	Phe	Leu	Arg	His	Ile	Glu	Arg	Thr	Ser	Val	Leu	
225					230					235					240	
Val	His	Val	Val	Asp	Thr	Ala	Thr	Met	Asp	Pro	Gly	Arg	Asp	Pro	Ile	
				245					250					255		
Ser	Asp	Ile	Glu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Ala	Tyr	Gln	Ser	Ala	
			260					265					270			
Leu	Asp	Glu	Asp	Thr	Gly	Leu	Gly	Asp	Leu	Ser	Gln	Arg	Pro	Arg	Leu	
	275						280					285				
Val	Val	Leu	Asn	Lys	Ala	Asp	Val	Pro	Glu	Ala	Glu	Glu	Leu	Ala	Glu	
	290					295					300					
Phe	Leu	Lys	Glu	Asp	Ile	Glu	Lys	Gln	Phe	Gly	Trp	Pro	Val	Phe	Ile	
305					310					315					320	
Ile	Ser	Ala	Val	Ala	Arg	Lys	Gly	Leu	Asp	Pro	Leu	Lys	Tyr	Lys	Leu	
				325					330					335		
Leu	Glu	Ile	Val	Gln	Asp	Ala	Arg	Lys	Lys	Arg	Pro	Lys	Glu	Lys	Ala	
			340					345					350			
Glu	Ser	Val	Ile	Ile	Lys	Pro	Lys	Ala	Val	Asp	His	Arg	Thr	Lys	Gly	
		355					360				365					
Gln	Phe	Gln	Ile	Lys	Pro	Asp	Pro	Glu	Val	Gln	Gly	Gly	Phe	Ile	Ile	
	370					375					380					
Thr	Gly	Glu	Lys	Pro	Glu	Arg	Trp	Ile	Leu	Gln	Thr	Asp	Phe	Glu	Asn	
385					390					395					400	
Asp	Glu	Ala	Val	Gly	Tyr	Leu	Ala	Asp	Arg	Leu	Ala	Lys	Leu	Gly	Ile	
				405					410					415		
Glu	Asp	Gly	Leu	Arg	Lys	Ala	Gly	Ala	His	Val	Gly	Ala	Asn	Val	Thr	
			420					425					430			
Ile	Gly	Gly	Ile	Ser	Phe	Glu	Trp	Glu	Pro	Met	Thr	Thr	Ala	Gly	Asp	
		435					440					445				
Asp	Pro	Val	Leu	Thr	Gly	Arg	Gly	Thr	Asp	Val	Arg	Leu	Glu	Gln	Thr	
	450					455					460					

Ser Arg Ile Ser Ala Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg
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Gly Leu Ile Asp Glu Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg
485 490 495

Glu Arg Trp Glu Gly
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<211> 605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(582)

<223> RXA01065

<400> 219

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atc atc acc aaa gca gac agc gtc tca cgt gac ttg gtt gcg gcc caa	96
Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln	
20 25 30	
ctg atg gct gtc cat gag ctg ctc ggc gga aac agc gag gta gtc cca	144
Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro	
35 40 45	
gtg tct tcc acc tcg ggg gaa aac gtc gaa acg ctt att aag gtc atg	192
Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met	
50 55 60	
acc gac ctg ctg cct gaa ggc ccc aag ttc tac ccg gat gat cac atc	240
Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile	
65 70 75 80	
acc gat gag gac acc aac acc cgc atc gcg gaa gcc atc cgc gaa gca	288
Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala	
85 90 95	
gca ctg tct ggc ttg aag aac gaa ctg ccg cac tcc gtc gca gtt gag	336
Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu	
100 105 110	
gtt gat gaa atc ctg cca gac cca gaa cgc aac ggt gtc ctg gct gtg	384
Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val	
115 120 125	
cac gcc atc atc tac gtc gag cgt gtt ggt cag aaa gac atc atc gtc	432
His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val	
130 135 140	
gga cac aag gga cag cgc ctg ggg cgc atc atc cac acc tca cgc caa	480
Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln	
145 150 155 160	

gac atc atc aag atc ctc ggc caa aac gta ttc ctt gac ctg cgc atc 528
 Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
 165 170 175

aag gtg ctg aag aac tgg caa tcc gat cca aag gct ttg aac cgc ctg 576
 Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
 180 185 190

ggc ttc tagctttaag ggggtgagtt cat 605
 Gly Phe

<210> 220

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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 35 40 45

Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
 50 55 60

Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65 70 75 80

Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
 85 90 95

Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
 100 105 110

Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
 115 120 125

His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
 130 135 140

Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
 145 150 155 160

Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
 165 170 175

Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
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Gly Phe

<210> 221

<211> 1650

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1627)

<223> RXA02232

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				Met	Asp	Glu	Lys	Lys	
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Asn	Leu	Ser	His	Asp	Glu	Leu	Leu	Ala	Gln	Ala	Phe	Arg	Gly	His	Lys	
			10					15						20		

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Asn	Thr	Val	Arg	Pro	Gly	Ser	Asp	Glu	Thr	Ser	Gly	Phe	Asp	Leu	Ser	
			25					30					35			

ggt	ttt	atc	cga	gct	gaa	gaa	cca	tca	act	ggt	gat	ctc	gac	cta	gag	259
Gly	Phe	Ile	Arg	Ala	Glu	Glu	Pro	Ser	Thr	Gly	Asp	Leu	Asp	Leu	Glu	
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Ala	Arg	Asp	Ala	Gln	Arg	Arg	Arg	Asp	Thr	Glu	Ile	His	Ala	Asp	Glu	
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gca	gca	gat	ggc	tac	gag	gtt	gag	tac	cga	aag	ctg	cga	ctt	gag	cgc	355
Ala	Ala	Asp	Gly	Tyr	Glu	Val	Glu	Tyr	Arg	Lys	Leu	Arg	Leu	Glu	Arg	
		70			75					80					85	

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Val	Ile	Leu	Val	Gly	Val	Trp	Thr	Glu	Gly	Thr	Thr	Ala	Glu	Ile	Asp	
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Ala	Ser	Leu	Ala	Glu	Leu	Ala	Ala	Leu	Ala	Asp	Thr	Ala	Gly	Ala	Glu	
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gtt	att	gaa	acg	ctg	tac	caa	aag	cgc	gat	aaa	cca	gat	cct	gga	acc	499
Val	Ile	Glu	Thr	Leu	Tyr	Gln	Lys	Arg	Asp	Lys	Pro	Asp	Pro	Gly	Thr	
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tac	att	ggt	tcc	ggc	aag	gtt	cgg	gag	tta	aag	gag	atc	atc	gaa	gcc	547
Tyr	Ile	Gly	Ser	Gly	Lys	Val	Arg	Glu	Leu	Lys	Glu	Ile	Ile	Glu	Ala	
		135				140					145					

act	agt	gca	gat	acc	gtg	gtg	tgc	gat	ggt	gaa	ctt	agc	cct	tcc	cag	595
Thr	Ser	Ala	Asp	Thr	Val	Val	Cys	Asp	Gly	Glu	Leu	Ser	Pro	Ser	Gln	
		150			155				160						165	

ctc	gtg	gca	tta	gag	cgc	gaa	ctt	gat	atc	aag	gtc	att	gac	cgc	acc	643
Leu	Val	Ala	Leu	Glu	Arg	Glu	Leu	Asp	Ile	Lys	Val	Ile	Asp	Arg	Thr	
			170					175						180		

atg	ctg	att	ctg	gat	atc	ttc	gcc	cag	cac	gct	aaa	tcg	cgc	gaa	ggt	691
Met	Leu	Ile	Leu	Asp	Ile	Phe	Ala	Gln	His	Ala	Lys	Ser	Arg	Glu	Gly	

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Lys	Ala	Gln	Val	Ala	Leu	Ala	Gln	Met	Glu	Tyr	Leu	Ile	Ser	Arg	Val				
200				205				210											
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Arg	Gly	Trp	Gly	Gly	Asn	Leu	Ser	Arg	Gln	Ala	Gly	Gly	Arg	Ala	Gly				
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Ser	Asn	Gly	Gly	Val	Gly	Leu	Arg	Gly	Pro	Gly	Glu	Thr	Lys	Ile	Glu				
230				235				240											
gca	gac	cg	cgt	cgt	ctt	cga	tcg	gat	atg	gct	cg	ctg	cg	agg	gaa	883			
Ala	Asp	Arg	Arg	Arg	Leu	Arg	Ser	Asp	Met	Ala	Arg	Leu	Arg	Arg	Glu				
250				255				260											
ctt	tcg	ggg	ctg	gat	acg	tcg	aga	agc	att	aaa	aga	gcg	caa	cg	gca	931			
Leu	Ser	Gly	Leu	Asp	Thr	Ser	Arg	Ser	Ile	Lys	Arg	Ala	Gln	Arg	Ala				
265				270				275											
gcc	tcc	ctg	gtg	ccg	cag	atc	gcc	atc	gct	ggc	tac	acg	aac	gcc	ggc	979			
Ala	Ser	Leu	Val	Pro	Gln	Ile	Ala	Ile	Ala	Gly	Tyr	Thr	Asn	Ala	Gly				
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aaa	tct	tcg	ctg	att	aac	gcg	atg	acc	ggc	gcg	ggg	gtg	ctg	gtg	gag	1027			
Lys	Ser	Ser	Leu	Ile	Asn	Ala	Met	Thr	Gly	Ala	Gly	Val	Leu	Val	Glu				
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Asn	Ala	Leu	Phe	Ala	Thr	Leu	Asp	Pro	Thr	Thr	Arg	Lys	Ala	Glu	Leu				
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Ala	Asp	Gly	Arg	His	Val	Val	Phe	Thr	Asp	Thr	Val	Gly	Phe	Val	Arg				
330				335				340											
cac	ctg	ccg	acc	tct	ctg	gtt	gag	gcg	ttc	aaa	tct	acg	ctg	gaa	gaa	1171			
His	Leu	Pro	Thr	Ser	Leu	Val	Glu	Ala	Phe	Lys	Ser	Thr	Leu	Glu	Glu				
345				350				355											
gtc	gtg	gag	gcg	gac	ctc	atg	ctg	cac	gtg	gtg	gat	gga	tcc	gat	ccg	1219			
Val	Val	Glu	Ala	Asp	Leu	Met	Leu	His	Val	Val	Asp	Gly	Ser	Asp	Pro				
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ttc	ccg	ctg	aag	cag	atc	gac	gct	gtg	aac	acc	gtg	att	agc	gat	att	1267			
Phe	Pro	Leu	Lys	Gln	Ile	Asp	Ala	Val	Asn	Thr	Val	Ile	Ser	Asp	Ile				
375				380				385											
gtg	cga	tcc	acc	ggg	gcg	gtg	cca	cca	cca	gag	atc	atc	gtg	gtg	aac	1315			
Val	Arg	Ser	Thr	Gly	Ala	Val	Pro	Pro	Pro	Glu	Ile	Ile	Val	Val	Asn				
390				395				400				405							
aaa	att	gac	caa	gct	gat	ccg	ctg	acg	ctg	gca	gaa	cta	cg	cac	gcc	1363			
Lys	Ile	Asp	Gln	Ala	Asp	Pro	Leu	Thr	Leu	Ala	Glu	Leu	Arg	His	Ala				
410				415				420											
gtc	gac	gat	gtg	gtg	ttt	gtc	tct	gcg	ctg	aca	ggg								

gag ctg gaa gct cgc atc gaa cta ttc ctc aac tcc agg gac gcg cac 1459
 Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn Ser Arg Asp Ala His
 440 445 450

cta ctg ctg aaa atc ccg ttc acc cgt ggc gat att gtg tcc cgc ctg 1507
 Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp Ile Val Ser Arg Leu
 455 460 465

cac cag cat ggc acc gtt ctc agc gaa gac tac gcc gaa gac ggc acc 1555
 His Gln His Gly Thr Val Leu Ser Glu Asp Tyr Ala Glu Asp Gly Thr
 470 475 480 485

ttg atg gat gtg cgt atc ccc acc caa ttg gcc caa gag ctg cag agt 1603
 Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala Gln Glu Leu Gln Ser
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 Tyr Val Val Glu Pro Thr Ser Ala
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<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Phe Arg Gly His Lys Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser
 20 25 30

Gly Phe Asp Leu Ser Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly
 35 40 45

Asp Leu Asp Leu Glu Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu
 50 55 60

Ile His Ala Asp Glu Ala Ala Asp Gly Tyr Glu Val Glu Tyr Arg Lys
 65 70 75 80

Leu Arg Leu Glu Arg Val Ile Leu Val Gly Val Trp Thr Glu Gly Thr
 85 90 95

Thr Ala Glu Ile Asp Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp
 100 105 110

Thr Ala Gly Ala Glu Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys
 115 120 125

Pro Asp Pro Gly Thr Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys
 130 135 140

Glu Ile Ile Glu Ala Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu
 145 150 155 160

Leu Ser Pro Ser Gln Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys
 165 170 175

Val Ile Asp Arg Thr Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala
 180 185 190
 Lys Ser Arg Glu Gly Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr
 195 200 205
 Leu Ile Ser Arg Val Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala
 210 215 220
 Gly Gly Arg Ala Gly Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly
 225 230 235 240
 Glu Thr Lys Ile Glu Ala Asp Arg Arg Arg Leu Arg Ser Asp Met Ala
 245 250 255
 Arg Leu Arg Arg Glu Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys
 260 265 270
 Arg Ala Gln Arg Ala Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly
 275 280 285
 Tyr Thr Asn Ala Gly Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala
 290 295 300
 Gly Val Leu Val Glu Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr
 305 310 315 320
 Arg Lys Ala Glu Leu Ala Asp Gly Arg His Val Val Phe Thr Asp Thr
 325 330 335
 Val Gly Phe Val Arg His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys
 340 345 350
 Ser Thr Leu Glu Glu Val Val Glu Ala Asp Leu Met Leu His Val Val
 355 360 365
 Asp Gly Ser Asp Pro Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr
 370 375 380
 Val Ile Ser Asp Ile Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu
 385 390 395 400
 Ile Ile Val Val Asn Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala
 405 410 415
 Glu Leu Arg His Ala Val Asp Asp Val Val Phe Val Ser Ala Leu Thr
 420 425 430
 Gly Glu Gly Ile Lys Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn
 435 440 445
 Ser Arg Asp Ala His Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp
 450 455 460
 Ile Val Ser Arg Leu His Gln His Gly Thr Val Leu Ser Glu Asp Tyr
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 Ala Glu Asp Gly Thr Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala
 485 490 495
 Gln Glu Leu Gln Ser Tyr Val Val Glu Pro Thr Ser Ala

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<213> Corynebacterium glutamicum

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<222> (1)..(171)
<223> RXA00848

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Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala
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Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val
20 25 30
ctg cgc atc cgc aag gtc atc ctg aac gct act gag cgt ggc cgt gca 144
Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
35 40 45
cgt tcc cgt gcg aag agc ctg aac aag taattctctt ttagttaaga gtt 194
Arg Ser Arg Ala Lys Ser Leu Asn Lys
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<210> 224
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<213> Corynebacterium glutamicum

<400> 224
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35 40 45
Arg Ser Arg Ala Lys Ser Leu Asn Lys
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 Met Pro Pro Val Thr
 1 5

cac cca gag ttt cgt aac gta gcg att gtc gcg cac gtt gac cac gga 163
 His Pro Glu Phe Arg Asn Val Ala Ile Val Ala His Val Asp His Gly
 10 15 20

aag acc aca ctc gtt aat gcc atg ctt gaa cag tct ggc gta ttc agt 211
 Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln Ser Gly Val Phe Ser
 25 30 35

gac cac ggt gaa gta gcc gac cgt gtg atg gac tcc ggt gac ctg gaa 259
 Asp His Gly Glu Val Ala Asp Arg Val Met Asp Ser Gly Asp Leu Glu
 40 45 50

aag gaa aag ggc atc acc atc ctt gcc aag aac acc gcg att cgt cgt 307
 Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Arg Arg
 55 60 65

aaa ggc gct ggc aag gac ggc aat gac ctg att atc aac gtc att gac 355
 Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile Ile Asn Val Ile Asp
 70 75 80 85

acc cca ggc cac gct gac ttc ggt ggc gaa gtt gag cgc gca ctg tcc 403
 Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val Glu Arg Ala Leu Ser
 90 95 100

atg gtt gac ggc gtt gtc ctt ctg gtt gac gca tct gaa ggc cca ctg 451
 Met Val Asp Gly Val Val Leu Leu Val Asp Ala Ser Glu Gly Pro Leu
 105 110 115

cct cag acc cga ttc gtg 469
 Pro Gln Thr Arg Phe Val
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<210> 226

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Pro Pro Val Thr His Pro Glu Phe Arg Asn Val Ala Ile Val Ala
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His Val Asp His Gly Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln
 20 25 30

Ser Gly Val Phe Ser Asp His Gly Glu Val Ala Asp Arg Val Met Asp
 35 40 45

Ser Gly Asp Leu Glu Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn
 50 55 60

Thr Ala Ile Arg Arg Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile
 65 70 75 80

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Ser	Ser	Phe	Leu	Gly	Arg	Ile	Gly	Leu	Val	Arg	Val	His	Ala	Gly	Thr	
1				5					10					15		
ttg	cgt	aag	ggc	cag	cag	gtt	gca	tgg	att	cac	tac	gat	gaa	gaa	ggt	96
Leu	Arg	Lys	Gly	Gln	Gln	Val	Ala	Trp	Ile	His	Tyr	Asp	Glu	Glu	Gly	
			20					25					30			
aac	cag	cac	acc	aag	acc	gct	aag	atc	gca	gag	ctt	ctg	gct	acc	gtt	144
Asn	Gln	His	Thr	Lys	Thr	Ala	Lys	Ile	Ala	Glu	Leu	Leu	Ala	Thr	Val	
		35					40					45				
ggc	gtt	gcc	cgc	gtt	cct	gct	acc	gaa	gtt	gtt	gca	ggg	gac	atc	gct	192
Gly	Val	Ala	Arg	Val	Pro	Ala	Thr	Glu	Val	Val	Ala	Gly	Asp	Ile	Ala	
	50					55					60					
gct	atc	tcc	ggc	atc	gaa	gac	atc	atg	att	ggc	gat	acc	ctc	gcg	gat	240
Ala	Ile	Ser	Gly	Ile	Glu	Asp	Ile	Met	Ile	Gly	Asp	Thr	Leu	Ala	Asp	
	65				70					75					80	
cct	gag	aac	cca	gtt	gca	ctg	cct	cgc	atc	acc	gtt	gat	gag	cca	gca	288
Pro	Glu	Asn	Pro	Val	Ala	Leu	Pro	Arg	Ile	Thr	Val	Asp	Glu	Pro	Ala	
				85					90					95		
ctg	tcc	atg	acc	atc	ggt	gtg	aac	acc	tca	cca	atg	gct	ggg	cgt	ggc	336
Leu	Ser	Met	Thr	Ile	Gly	Val	Asn	Thr	Ser	Pro	Met	Ala	Gly	Arg	Gly	
			100					105					110			
ggc	gga	gac	aag	ctg	acc	gca	cgt	gtg	gtc	aag	gct	cgt	ctt	gag	aac	384
Gly	Gly	Asp	Lys	Leu	Thr	Ala	Arg	Val	Val	Lys	Ala	Arg	Leu	Glu	Asn	
		115					120					125				
gaa	ctg	atc	ggt	aac	gtg	tcc	ctg	aag	gtc	aac	cca	act	gag	cgc	cca	432
Glu	Leu	Ile	Gly	Asn	Val	Ser	Leu	Lys	Val	Asn	Pro	Thr	Glu	Arg	Pro	
	130					135					140					
gat	acc	tgg	gaa	gtt	cag	ggt	cgt	ggc	gaa	atg	gct	ctg	tcc	atc	ctc	480
Asp	Thr	Trp	Glu	Val	Gln	Gly	Arg	Gly	Glu	Met	Ala	Leu	Ser	Ile	Leu	
145					150					155					160	

gtt gag acc atg cgt cgc gaa ggc ttc gag ctc acc gtt ggt aag cca 528
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
 165 170 175

cag gtt gtt acc cag acc atc gac ggc aag ctg cac gag cct tac gag 576
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
 180 185 190

atc atc gtc atc gac gtt cct tcc gag tac cag ggc aac gtg acc cag 624
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
 195 200 205

ctg ctg gct acc cgc aag ggc ctc atg cag tcc atg tcc acc acc cca 672
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
 210 215 220

ggt tcc gac tgg atc cgc atg gaa ttc cgt att cct gct cgt ggc ctg 720
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
 225 230 235 240

att ggt ttc cgt acc cag ttc atg act gaa acc cgt ggt acc ggt atc 768
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
 245 250 255

gct aac tcc tac tct gac ggc atg gat gtt tgg gct ggc gaa atc aag 816
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
 260 265 270

ggc cgc gca cac ggt tcc ttg gtt gct gac cgt tcc ggc cag atc acc 864
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
 275 280 285

gct tac gct ctg acc cag ctg gca gac cgt ggt agc ttc 903
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe
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<210> 228

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Ser Ser Phe Leu Gly Arg Ile Gly Leu Val Arg Val His Ala Gly Thr
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Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly
 20 25 30

Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val
 35 40 45

Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala
 50 55 60

Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp
 65 70 75 80

Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala
 85 90 95

Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly
 100 105 110
 Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn
 115 120 125
 Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro
 130 135 140
 Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu
 145 150 155 160
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
 165 170 175
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
 180 185 190
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
 195 200 205
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
 210 215 220
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
 225 230 235 240
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
 245 250 255
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
 260 265 270
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
 275 280 285
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe
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<210> 229

<211> 581

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (19)..(558)

<223> RXA02365

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 ggt ggc atg gac tac ctt tcg gag gac cgc gtg gag ctg cgc tac acc 99
 Gly Gly Met Asp Tyr Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr 15 20 25
 atg cct ttg ggt gag atc atc ttt gac ttc ttc gat atg ttg aag tct 147
 Met Pro Leu Gly Glu Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser

30	35	40	
cgc acc aag ggt tac gct tcg ctg aac tac gag gaa gct ggc gag cag			195
Arg Thr Lys Gly Tyr Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln			
45	50	55	
act gcc gac ctg gtc aag gta gat atc ttg ctc caa ggt gaa cct gtg			243
Thr Ala Asp Leu Val Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val			
60	65	70	75
gat gca ttc tct gcg atc gtg cac cgc gat aat gcg cag tgg tac gga			291
Asp Ala Phe Ser Ala Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly			
	80	85	90
aac aag atg act gtg aag ctg aag gaa ctg atc cct cgc cag cag ttc			339
Asn Lys Met Thr Val Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe			
	95	100	105
gaa gtt cct gtg cag gca gcc att ggt tcc aag gtt atc gct cgt gaa			387
Glu Val Pro Val Gln Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu			
	110	115	120
aac att cgt gca ctg cgc aag gac gtg ttg gcg aag tgt tac ggt ggc			435
Asn Ile Arg Ala Leu Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly			
	125	130	135
gat att tcc cgt aag cgc aag ctt ctg gaa aag cag aag gct ggt aag			483
Asp Ile Ser Arg Lys Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys			
	140	145	150
aag cgc atg aag aac atc ggt tcg gtc gag gtt cct cag gaa gca ttc			531
Lys Arg Met Lys Asn Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe			
	160	165	170
gta gca gca ctg tct acc gac gag gca taaaaaactt tagcctcttt tag			581
Val Ala Ala Leu Ser Thr Asp Glu Ala			
	175	180	

<210> 230

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

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Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr Met Pro Leu Gly Glu			
	20	25	30
Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser Arg Thr Lys Gly Tyr			
	35	40	45
Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln Thr Ala Asp Leu Val			
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Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val Asp Ala Phe Ser Ala			
	65	70	75
			80

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																Met Ala Glu Lys Phe	5
																1	
gca gaa aca aca ttt acg gat cca gcc agg att cgt aac ttc tgc atc																163	
Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile Arg Asn Phe Cys Ile																	
																10 15 20	
att gcc cac att gac cac ggt aaa tct acg ctc gct gac cgt atc ctg																211	
Ile Ala His Ile Asp His Gly Lys Ser Thr Leu Ala Asp Arg Ile Leu																	
																25 30 35	
cag ctg tct aac gtt gtg gat gcc cgc gat atg cgt gat cag tac ctg																259	
Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met Arg Asp Gln Tyr Leu																	
																40 45 50	
gac aac atg gac atc gaa cgt gaa cgt ggc att acc att aag gct cag																307	
Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala Gln																	
																55 60 65	
aac gtt cgc ctg cca tgg att cct cgc agt ggt gag tac gag ggc cag																355	
Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly Glu Tyr Glu Gly Gln																	
																70 75 80 85	
cag atc gtc atg cag atg atc gat acg cca ggc cac gtg gac ttc acc																403	
Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly His Val Asp Phe Thr																	

90							95						100					
tat	gaa	gtg	tct	cgg	gcg	ctt	gaa	gcg	tgt	gaa	ggc	gcg	att	ttg	ctt	451		
Tyr	Glu	Val	Ser	Arg	Ala	Leu	Glu	Ala	Cys	Glu	Gly	Ala	Ile	Leu	Leu			
105							110						115					
gtt	gat	gca	gcg	cag	ggc	att	gaa	gcc	cag	acc	ttg	gca	aac	ttg	tat	499		
Val	Asp	Ala	Ala	Gln	Gly	Ile	Glu	Ala	Gln	Thr	Leu	Ala	Asn	Leu	Tyr			
120							125						130					
ttg	gct	atg	gaa	aac	gat	ctt	gag	atc	atc	cct	gtg	ctg	aac	aag	att	547		
Leu	Ala	Met	Glu	Asn	Asp	Leu	Glu	Ile	Ile	Pro	Val	Leu	Asn	Lys	Ile			
135							140						145					
gac	ctt	cca	gcg	gcg	gat	cca	gac	aag	tac	gcg	ttg	gag	atc	gcc	aac	595		
Asp	Leu	Pro	Ala	Ala	Asp	Pro	Asp	Lys	Tyr	Ala	Leu	Glu	Ile	Ala	Asn			
150							155						160					
att	gtg	ggc	tgt	gaa	cct	gaa	gat	gtg	ttg	cgc	gtg	tcc	ggc	aaa	act	643		
Ile	Val	Gly	Cys	Glu	Pro	Glu	Asp	Val	Leu	Arg	Val	Ser	Gly	Lys	Thr			
170							175						180					
ggc	atg	ggc	gtc	cct	gag	ctt	ctg	gat	aag	gtc	gtt	gaa	ctt	atc	cca	691		
Gly	Met	Gly	Val	Pro	Glu	Leu	Leu	Asp	Lys	Val	Val	Glu	Leu	Ile	Pro			
185							190						195					
gca	cct	acc	tct	gaa	ttt	gag	gaa	gac	gcc	cca	gct	cgt	gcg	atg	att	739		
Ala	Pro	Thr	Ser	Glu	Phe	Glu	Glu	Asp	Ala	Pro	Ala	Arg	Ala	Met	Ile			
200							205						210					
ttc	gac	tct	gtc	tat	gac	acc	tac	cgc	ggc	gtg	gtt	acc	tac	atc	cgc	787		
Phe	Asp	Ser	Val	Tyr	Asp	Thr	Tyr	Arg	Gly	Val	Val	Thr	Tyr	Ile	Arg			
215							220						225					
atg	atg	gac	ggc	aag	ctg	aca	cct	cgc	caa	aag	atc	aag	atg	atg	tcc	835		
Met	Met	Asp	Gly	Lys	Leu	Thr	Pro	Arg	Gln	Lys	Ile	Lys	Met	Met	Ser			
230							235						240					
acc	ggc	gcc	acc	cac	gag	ttg	ctg	gaa	atc	ggc	atc	gtg	agc	ccc	acc	883		
Thr	Gly	Ala	Thr	His	Glu	Leu	Leu	Glu	Ile	Gly	Ile	Val	Ser	Pro	Thr			
250							255						260					
cct	aaa	aag	tgt	gtg	ggc	ctt	gga	cct	ggc	gag	gtt	ggc	tac	ctg	atc	931		
Pro	Lys	Lys	Cys	Val	Gly	Leu	Gly	Pro	Gly	Glu	Val	Gly	Tyr	Leu	Ile			
265							270						275					
acc	ggc	gtg	aag	gac	gtg	cgc	caa	tct	aag	gtg	ggc	gat	acc	gtc	acg	979		
Thr	Gly	Val	Lys	Asp	Val	Arg	Gln	Ser	Lys	Val	Gly	Asp	Thr	Val	Thr			
280							285						290					
tg	gca	att	cat	gga	gct	gag	cag	cca	ctg	cgc	ggc	tac	cag	gaa	cca	1027		
Trp	Ala	Ile	His	Gly	Ala	Glu	Gln	Pro	Leu	Arg	Gly	Tyr	Gln	Glu	Pro			
295							300						305					
aca	ccg	atg	gtt	tac	tcg	ggc	ttg	ttc	ccg	att	tcc	caa	gcg	gat	ttc	1075		
Thr	Pro	Met	Val	Tyr	Ser	Gly	Leu	Phe	Pro	Ile	Ser	Gln	Ala	Asp	Phe			
310							315						320					
ccc	gac	ttg	cgc	gat	gcg	ctt	gaa	aag	ctg	cag	ctt	aac	gac	gcc	tcc	1123		
Pro	Asp	Leu	Arg	Asp	Ala	Leu	Glu	Lys	Leu	Gln	Leu	Asn	Asp	Ala	Ser			

ctc acg tac gaa ccc gaa acg tcc gta gca ctg ggc ttt ggt ttc cga 1171
 Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu Gly Phe Gly Phe Arg
 345 350 355

tgt ggc ttc ctc gga ctg ctg cac atg gaa atc acc cgt gac cga ctc 1219
 Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile Thr Arg Asp Arg Leu
 360 365 370

gaa cgt gag ttt ggc ctt gat ctg att tct acc gcg cca tct gtt aac 1267
 Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr Ala Pro Ser Val Asn
 375 380 385

tac cgc gtt att gat gag gcg ggc aag gaa ttc cgc gtc cac aac cca 1315
 Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe Arg Val His Asn Pro
 390 395 400 405

tct gac tgg cct ggc gga aag ctc agt gaa gtt tac gag ccc atc 1360
 Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val Tyr Glu Pro Ile
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<210> 232

<211> 420

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ala Glu Lys Phe Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile
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Arg Asn Phe Cys Ile Ile Ala His Ile Asp His Gly Lys Ser Thr Leu
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Ala Asp Arg Ile Leu Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met
 35 40 45

Arg Asp Gln Tyr Leu Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile
 50 55 60

Thr Ile Lys Ala Gln Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly
 65 70 75 80

Glu Tyr Glu Gly Gln Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly
 85 90 95

His Val Asp Phe Thr Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu
 100 105 110

Gly Ala Ile Leu Leu Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr
 115 120 125

Leu Ala Asn Leu Tyr Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro
 130 135 140

Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala
 145 150 155 160

Leu Glu Ile Ala Asn Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg
 165 170 175

Val Ser Gly Lys Thr Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val
 180 185 190
 Val Glu Leu Ile Pro Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro
 195 200 205
 Ala Arg Ala Met Ile Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val
 210 215 220
 Val Thr Tyr Ile Arg Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys
 225 230 235 240
 Ile Lys Met Met Ser Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly
 245 250 255
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 260 265 270
 Val Gly Tyr Leu Ile Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val
 275 280 285
 Gly Asp Thr Val Thr Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg
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 Gly Tyr Gln Glu Pro Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile
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 Ser Gln Ala Asp Phe Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln
 325 330 335
 Leu Asn Asp Ala Ser Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu
 340 345 350
 Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile
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 Thr Arg Asp Arg Leu Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr
 370 375 380
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<211> 2205

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA01573

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Arg Ala Ala Leu Val Val Val Ala Thr Thr Ala Val Ser Phe Ser Ala		
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Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser Asn Val Glu Leu Asn		
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Ile Leu Gly Val Thr Asp Phe His Gly His Ile Glu Gln Lys Ala Val		
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Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser Glu Met Gly Ala Ser		
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Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala Asp Asn Pro Asn Thr		
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cgc ttc atc acc gtt ggt gac aac att ggt gga tcc cca ttc gtg tcc		403
Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly Ser Pro Phe Val Ser		
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tcc atc ctg aag gat gag cca acc ttg caa gcc ctc agc gcc atc ggt		451
Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala Leu Ser Ala Ile Gly		
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Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe Asp Gln Gly Tyr Ser		
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Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser Gly Ser Ala Lys Phe		
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Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr Pro Ala Pro Ala Lys		
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Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile Ala Tyr Val Gly Ala		
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gta acc gag gag acc gca acc ttg gtc tcc cca gca ggc atc gaa ggc		691
Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro Ala Gly Ile Glu Gly		
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Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn Ala Glu Ala Asp Arg		
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Ser Gly His Thr His Phe Asp Tyr Val Ala Glu Gly Glu Ala Arg Gly	
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Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile Gly Ile Met Asn Ala	
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Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg Ile Thr His Ile Thr	
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Phe 470	Asn	Gly	Glu	Pro	Met 475	Asp	Met	Lys	Glu	Thr 480	Tyr	Arg	Val	Thr	Gly 485	
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Ser	Val	Gly	Ile	Ala	Leu	Ser 540	Gly	Pro	Ala	Val	Ala	Glu	Asp	Gly	Thr	
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Gln	Ser	Ser	Gly	Ser 650	Ser	Asp	Ala	Gly	Ser 655	Leu	Val	Ala	Val	Leu 660	Gly	
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Val	Leu	Gly	Ala 665	Leu	Gly	Gly	Leu 670	Val	Ala	Phe	Phe	Leu 675	Asn	Ser	Ala	
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Gln	Gly	Ala	Pro	Phe	Leu	Ala	Gln 685	Leu	Gln	Ala	Met	Phe 690	Ala	Gln	Phe	
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

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Glu Gln Lys Ala Val Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser
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Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala
 65           70           75           80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly
          85           90           95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala
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Leu Ser Ala Ile Gly Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe
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Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser
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Gly Ser Ala Lys Phe Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr
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Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile
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Ala Tyr Val Gly Ala Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro
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Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn
 195           200           205

Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
 210           215           220

Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn
 225           230           235           240

Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu
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Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His
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Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu
 275           280           285

Ala Gly Lys Ile Thr Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp
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 Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr
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 Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu
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 Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile
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 Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu
 385 390 395 400
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 405 410 415
 Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln
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 Gln Trp Lys Glu Thr Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser
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 Arg Ala Asn Gln Ser Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val
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 545 550 555 560
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 565 570 575
 Val Thr Val Gly Thr Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile
 580 585 590
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 610 615 620

Phe Glu Leu Pro Val Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp
 625 630 635 640
 Asp Asp Lys Glu Gln Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu
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 Met Phe Ala Gln Phe Met
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 <223> RXN01445

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 Met Ile Pro Leu Ile
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 Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
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 Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
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 Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
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 Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
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 Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
 70 75 80 85
 att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa 403
 Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
 90 95 100
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 Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
 105 110 115

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Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
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Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
135 140 145

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Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
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Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
170 175 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca 691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
185 190 195

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Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
200 205 210

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Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
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gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc 835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
230 235 240 245

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Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
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Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
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Gly	Arg	Phe	Ala	Leu	Ala	Leu	Ile	Leu	Gly	Val	Glu	Trp	Ile	Leu	Ile	50	55	60	
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His	Asp	Ser	Met	Ala	Arg	Ser	Leu	Ala	Ile	Met	Ile	Val	Gln	Ser	Lys	130	135	140	
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Val	Arg	His	Leu	Val	Val	Glu	Glu	Ser	Ala	Glu	Lys	Ala	Thr	Ala	Phe	180	185	190	
Gly	Ala	Trp	Ala	Ala	Val	Ser	Ile	His	Asp	Thr	Val	Asn	Ser	Ala	Ile	195	200	205	
Gln	Leu	Leu	Val	Asp	Ala	Gly	His	Val	Val	Ser	Phe	Asp	Ser	Arg	Lys	210	215	220	
Lys	Asn	Tyr	Lys	Leu	Asp	His	Ile	Ala	Glu	Thr	Ala	Phe	Ala	Leu	Ala	225	230	235	240
Phe	Asn	Glu	Ala	Val	Cys	Asn	Ala	Ile	Lys	His	Ser	Pro	Pro	Lys	Ala	245	250	255	
Asn	Val	Thr	Ile	Arg	Ile	Thr	Glu	Lys	Ala	Gln	Ser	Leu	Gln	Ile	Leu	260	265	270	
Val	Met	Asn	Pro	Ile	Gly	Asp	Trp	His	Ala	Asn	Gly	Glu	Ser	Ala	Ile	275	280	285	
Pro	Gly	Val	Gly	Ile	Gly	Val	Glu	Ser	Leu	Thr	Arg	Arg	Ile	Arg	Asn	290	295	300	
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Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp Ala Arg Ala Ser Ala 165																

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Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala Glu Arg Ala Arg Ile	
170 175 180	
gcg ggc gaa ata cat gac act gtg gcg cag ggg ttg tcc tcg att cag	691
Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln	
185 190 195	
atg ttg ttg cat gcg gcg gaa aaa cgg gtg gat gat ccg cag gcg tta	739
Met Leu Leu His Ala Ala Glu Lys Arg Val Asp Asp Pro Gln Ala Leu	
200 205 210	
agc cat ata cgg ttg gcc agg caa acg aca gct gat aat ttg gcg gag	787
Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala Asp Asn Leu Ala Glu	
215 220 225	
acc agg cag atc att gct gcg ctg caa ccg act cca ctc att ggg gcg	835
Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr Pro Leu Ile Gly Ala	
230 235 240 245	
gat ctg ccg gtg gcg ttg gcc aga ctg tcg tcg acc acc ccg atg gga	883
Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser Thr Thr Pro Met Gly	
250 255 260	
cag aac atc acg ttt gaa gtc gac gga tcc cca cgg gta tta cct gat	931
Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro Arg Val Leu Pro Asp	
265 270 275	
gcg atg gag gca gag atc gta cga att gcc caa acg ctg ctg gga aat	979
Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln Thr Leu Leu Gly Asn	
280 285 290	
gtg gtg cgg cat gca cag gca gat tct gca aaa atg acc ctg aca tat	1027
Val Val Arg His Ala Gln Ala Asp Ser Ala Lys Met Thr Leu Thr Tyr	
295 300 305	
caa gat gat caa ata ctt cta gat gtc atc gat aat ggg cag gga ttt	1075
Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp Asn Gly Gln Gly Phe	
310 315 320 325	
gat gtg gca gaa gtg atc cgt aaa aaa tcc att gga ctg ccc aca gcg	1123
Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile Gly Leu Pro Thr Ala	
330 335 340	
caa cgc cgg gct gaa ggg ctg ggc gga aca ata att att gaa tct aca	1171
Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile Ile Ile Glu Ser Thr	
345 350 355	
atc gga tcg gga act gga att tcc gcc cgt ttt ccc tat cca caa aag	1219
Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe Pro Tyr Pro Gln Lys	
360 365 370	
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Asp Gln Asp Lys	
375	

<210> 238

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Trp	Gly	Leu	His	Leu	Leu	Ile	Ala	Val	Leu	Leu	Val	Leu	Val	Cys	Trp	20	25	30	
Arg	Ala	Ser	His	Trp	Gly	Val	Trp	Val	Leu	Ala	Phe	Gly	Tyr	Gly	Val	35	40	45	
Val	Tyr	Val	Ala	Gly	Val	Val	Pro	Asn	Ser	Pro	Phe	Lys	Asn	His	Pro	50	55	60	
Met	Ala	Trp	Phe	Leu	Val	Leu	Ser	Leu	Leu	Trp	Ala	Ser	Leu	Ile	Trp	65	70	75	80
Asp	Gly	Pro	Glu	Pro	Ala	Tyr	Leu	Val	Phe	Pro	Met	Phe	Phe	Leu	Ala	85	90	95	
Val	Leu	Ile	Thr	Thr	Pro	Leu	Lys	Ser	Ala	Ile	Ile	Ile	Ala	Ile	Leu	100	105	110	
Thr	Ala	Ile	Ala	Val	Val	Thr	Leu	Ala	Met	His	Leu	Gly	Phe	Ser	Val	115	120	125	
Gly	Val	Val	Thr	Gly	Pro	Ile	Leu	Gly	Ala	Leu	Val	Ala	Trp	Val	Met	130	135	140	
Gly	Thr	Cys	Phe	Gln	Leu	Ala	Gln	Ala	Leu	Lys	Glu	Leu	Val	Asp		145	150	155	160
Ala	Arg	Ala	Ser	Ala	Ile	Arg	Ala	Ser	Lys	Ser	Ala	Gly	Glu	Gln	Ala	165	170	175	
Glu	Arg	Ala	Arg	Ile	Ala	Gly	Glu	Ile	His	Asp	Thr	Val	Ala	Gln	Gly	180	185	190	
Leu	Ser	Ser	Ile	Gln	Met	Leu	Leu	His	Ala	Ala	Glu	Lys	Arg	Val	Asp	195	200	205	
Asp	Pro	Gln	Ala	Leu	Ser	His	Ile	Arg	Leu	Ala	Arg	Gln	Thr	Thr	Ala	210	215	220	
Asp	Asn	Leu	Ala	Glu	Thr	Arg	Gln	Ile	Ile	Ala	Ala	Leu	Gln	Pro	Thr	225	230	235	240
Pro	Leu	Ile	Gly	Ala	Asp	Leu	Pro	Val	Ala	Leu	Ala	Arg	Leu	Ser	Ser	245	250	255	
Thr	Thr	Pro	Met	Gly	Gln	Asn	Ile	Thr	Phe	Glu	Val	Asp	Gly	Ser	Pro	260	265	270	
Arg	Val	Leu	Pro	Asp	Ala	Met	Glu	Ala	Glu	Ile	Val	Arg	Ile	Ala	Gln	275	280	285	
Thr	Leu	Leu	Gly	Asn	Val	Val	Arg	His	Ala	Gln	Ala	Asp	Ser	Ala	Lys	290	295	300	
Met	Thr	Leu	Thr	Tyr	Gln	Asp	Asp	Gln	Ile	Leu	Leu	Asp	Val	Ile	Asp				

305 310 315 320
 Asn Gly Gln Gly Phe Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile
 325 330 335
 Gly Leu Pro Thr Ala Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile
 340 345 350
 Ile Ile Glu Ser Thr Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe
 355 360 365
 Pro Tyr Pro Gln Lys Asp Gln Asp Lys
 370 375

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 <211> 362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(339)
 <223> RXN03071

<400> 239
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 aac gag cag atc acc gaa gcc ttc gag cgc gac gtc gtc cca tac gcg 96
 Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
 20 25 30

 gag ctt ttc gac gcc tcc ggc cag att cct tca tcg cag gag ttc ttc 144
 Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe
 35 40 45

 cgc gtg tca ctc acc gga cag tat ctt cca gac agt gag gtt ttg ctg 192
 Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
 50 55 60

 cgc ctt cgc ccc gtc gac tcc ggc cca gca ttc caa tcg tta acc ccc 240
 Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
 65 70 75 80

 ttc gaa ctt gaa aac gga cag att gtc ctc gtc aac cgt ggt tac gaa 288
 Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
 85 90 95

 tca tca gag ggc aca atc gtc cca gag atc gag cct gct cct tca cac 336
 Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His
 100 105 110

 cag taaccatcac cggattcgcc gca 362
 Gln

<210> 240
 <211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Leu Ala Pro Trp Gln Leu His Lys Asp Asp Asp Ile Val Ala Arg
 1 5 10 15

Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
 20 25 30

Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe
 35 40 45

Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
 50 55 60

Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
 65 70 75 80

Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
 85 90 95

Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His
 100 105 110

Gln

<210> 241

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN03072

<400> 241

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ggattcgccg caagaacgag ggcctccagg ttctgcacct atg gaa gac agc ggc 115
 Met Glu Asp Ser Gly
 1 5

tac acc cag gtc tac gga att aac acc gaa cag atc agt gac gtc acc 163
 Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln Ile Ser Asp Val Thr
 10 15 20

ggc ctt gat ctt ggc acc gac tac gtc cag gtc gca gaa ggc gaa cct 211
 Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val Ala Glu Gly Glu Pro
 25 30 35

ggt gtt ttg aac cca atg cca ctg cct caa atg gac cgc ggt aac cac 259
 Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met Asp Arg Gly Asn His
 40 45 50

ctc tca tac ggc ttc cag tgg atc gcc ttc ggc atc atg gca cct tta 307
 Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly Ile Met Ala Pro Leu
 55 60 65

ggg ctt gga tac ttc atc tgg gct gaa atg cgc gaa cga cgc cgc gac 355
 Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg Glu Arg Arg Arg Asp
 70 75 80 85

aaa gca gaa cgc gaa cag atg gcc gag cta aac act ctt gaa cca gtg 403
 Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn Thr Leu Glu Pro Val
 90 95 100

gtg gaa acc cct gaa gtt gtt gaa act gca gaa cca acc atc acc ccg 451
 Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu Pro Thr Ile Thr Pro
 105 110 115

gct gca tcc aaa cga cgt tca cgc tac ggc gat caa cac cgc aat cac 499
 Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp Gln His Arg Asn His
 120 125 130

tac gag aag atc tcc aaa cga gac caa gag cgc ttc taagcccgtc 545
 Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg Phe
 135 140 145

tcatttttgc acc 558

<210> 242

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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 20 25 30

Ala Glu Gly Glu Pro Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met
 35 40 45

Asp Arg Gly Asn His Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly
 50 55 60

Ile Met Ala Pro Leu Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg
 65 70 75 80

Glu Arg Arg Arg Asp Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn
 85 90 95

Thr Leu Glu Pro Val Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu
 100 105 110

Pro Thr Ile Thr Pro Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp
 115 120 125

Gln His Arg Asn His Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg
 130 135 140

Phe

145

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 <223> RXN01773

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 Met Thr Val Asp Leu
 1 5
 tac cag gca cgc att cct ttt cag cgc gat ggc gtg cgc ttt gat cat 163
 Tyr Gln Ala Arg Ile Pro Phe Gln Arg Asp Gly Val Arg Phe Asp His
 10 15 20
 acg atg atc acc cac att caa gcc ggc ctg cat ctt ggt ggc tgc cgc 211
 Thr Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg
 25 30 35
 gca gca ggt tta ctg cct ata cca gca cat att gat cat att gtg cgc 259
 Ala Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg
 40 45 50
 ctg aca gcc gca gat ttc tat gac acc cag tca gca ccg cag ctg ctc 307
 Leu Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu
 55 60 65
 agc aac act gtg ctt gat gta ttg gac acc acc act caa gac ttg aag 355
 Ser Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys
 70 75 80 85
 gca ttg tgg cct gtt gca gaa cat att gct aca acc att cct gaa tct 403
 Ala Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser
 90 95 100
 gag aac gtg ctt atc cac tgc cag atg ggt atc aac cgc tca gct gca 451
 Glu Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala
 105 110 115
 ctc atg aca cgg gtg ttg atg ttg cgc aac gat tgc acc gcc gat gaa 499
 Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu
 120 125 130
 gca att gca ctg ctg cgt gat cga cgc tca ccg ttt gta ctg ttc aat 547
 Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro Phe Val Leu Phe Asn
 135 140 145
 gag cat ttt gtg gaa caa ctt cga gca ctg taagcgctca aagaccatt acc 600
 Glu His Phe Val Glu Gln Leu Arg Ala Leu
 150 155

<210> 244
 <211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

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Val Arg Phe Asp His Thr Met Ile Thr His Ile Gln Ala Gly Leu His
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Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro Ala His Ile
          35          40          45
Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser
          50          55          60
Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu Asp Thr Thr
          65          70          75          80
Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His Ile Ala Thr
          85          90          95
Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln Met Gly Ile
          100         105         110
Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp
          115         120         125
Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro
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Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg Ala Leu
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<210> 245

<211> 1344

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1321)

<223> RXN03090

<400> 245

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gggacgacga ctaactaacc cctgaggcac tttctatttc atg gct aaa tca act 115
                                         Met Ala Lys Ser Thr
                                         1           5
cct ttg att gca tcg cta cgc tgg cga att gtc ctg tgg atg aca gcg 163
Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val Leu Trp Met Thr Ala
          10          15          20
gtt gtt ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg 211
Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val
          25          30          35
ctg ctt tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa 259

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Leu	Leu	Ser	Glu	Val	Thr	Asn	Thr	Ala	Asn	Ser	Ala	Val	Glu	Gln	Glu		
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att	gag	gag	ttt	cgt	cgc	ttt	gca	gcc	gaa	gga	att	gat	cca	aca	act	307	
Ile	Glu	Glu	Phe	Arg	Arg	Phe	Ala	Ala	Glu	Gly	Ile	Asp	Pro	Thr	Thr		
	55					60					65						
gcg	cag	cct	ttt	gag	tca	ggt	cat	cgc	ctg	atg	gag	gtt	tac	ctg	tcg	355	
Ala	Gln	Pro	Phe	Glu	Ser	Gly	His	Arg	Leu	Met	Glu	Val	Tyr	Leu	Ser		
	70				75				80						85		
agg	cag	att	ccg	gat	gaa	aat	gaa	gcc	att	gtc	ggc	att	ttc	ccc	gga	403	
Arg	Gln	Ile	Pro	Asp	Glu	Asn	Glu	Ala	Ile	Val	Gly	Ile	Phe	Pro	Gly		
				90					95					100			
gag	ctc	att	cag	gtt	gat	tac	tcc	cag	ctc	agt	ggc	gcc	cat	ccg	ctt	451	
Glu	Leu	Ile	Gln	Val	Asp	Tyr	Ser	Gln	Leu	Ser	Gly	Ala	His	Pro	Leu		
			105					110					115				
cct	ttg	gaa	cac	tcc	gat	ccg	ttg	att	tcg	gaa	atc	cga	cag	acc	acg	499	
Pro	Leu	Glu	His	Ser	Asp	Pro	Leu	Ile	Ser	Glu	Ile	Arg	Gln	Thr	Thr		
		120					125					130					
ctg	aat	tct	gga	gtt	ttc	agc	gat	ctt	gaa	cgc	gga	acc	act	cac	tgg	547	
Leu	Asn	Ser	Gly	Val	Phe	Ser	Asp	Leu	Glu	Arg	Gly	Thr	Thr	His	Trp		
	135					140					145						
gga	aag	gtg	aat	ttc	caa	act	gct	tcc	ggt	gag	gcc	gat	ggt	gag	ttc	595	
Gly	Lys	Val	Asn	Phe	Gln	Thr	Ala	Ser	Gly	Glu	Ala	Asp	Gly	Glu	Phe		
	150			155					160						165		
gtt	gtc	gca	ttc	ttc	gct	gat	aat	ctt	aaa	gac	cag	gtc	aac	ggc	cag	643	
Val	Val	Ala	Phe	Phe	Ala	Asp	Asn	Leu	Lys	Asp	Gln	Val	Asn	Gly	Gln		
				170				175						180			
atc	cag	att	ctt	att	ttg	atc	ggc	aca	ggg	ggt	ttg	att	gcc	tca	att	691	
Ile	Gln	Ile	Leu	Ile	Leu	Ile	Gly	Thr	Gly	Gly	Leu	Ile	Ala	Ser	Ile		
			185					190					195				
ctg	att	gct	tgg	ttg	att	gcg	ggc	cag	atc	att	gcc	ccg	atc	cgc	aaa	739	
Leu	Ile	Ala	Trp	Leu	Ile	Ala	Gly	Gln	Ile	Ile	Ala	Pro	Ile	Arg	Lys		
		200					205					210					
ttg	agt	tcc	gtg	tcc	gca	aag	atc	agt	aat	tcg	gat	ctc	acc	tgg	cgc	787	
Leu	Ser	Ser	Val	Ser	Ala	Lys	Ile	Ser	Asn	Ser	Asp	Leu	Thr	Trp	Arg		
	215					220					225						
gtc	cct	gtg	gag	ggt	cgt	gat	gag	att	gcg	cag	ctg	gcc	agg	act	ttt	835	
Val	Pro	Val	Glu	Gly	Arg	Asp	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Thr	Phe		
	230				235					240					245		
aat	gcc	atg	ttg	gat	cgc	atc	gaa	atc	gcg	tat	aac	gat	cag	cgc	cag	883	
Asn	Ala	Met	Leu	Asp	Arg	Ile	Glu	Ile	Ala	Tyr	Asn	Asp	Gln	Arg	Gln		
				250					255					260			
ttc	gtt	gat	gat	gcc	ggc	cac	gag	ctg	cgc	acc	ccg	atc	aca	gtg	gtg	931	
Phe	Val	Asp	Asp	Ala	Gly	His	Glu	Leu	Arg	Thr	Pro	Ile	Thr	Val	Val		
			265					270					275				
cgt	ggc	cag	tta	gag	ctt	ctc	gcc	acc	acc	ccg	ccg	gag	gaa	caa	gcg	979	
Arg	Gly	Gln	Leu	Glu	Leu	Leu	Ala	Thr	Thr	Pro	Pro	Glu	Glu	Gln	Ala		

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Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile			
310	315 320 325		
cac gcc cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac		1123	
His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp			
	330 335 340		
aaa gcc cgc acc atc agc gac cga att ttg ctt gtc gac gcc cgc ccg		1171	
Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Arg Pro			
	345 350 355		
agg gcc tcg tca gcc tcg acg agc agc ggg tca ccg agg cag tgc ttg		1219	
Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser Pro Arg Gln Cys Leu			
	360 365 370		
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Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp Val Val Glu Leu			
	375 380 385		
ggt tca gga ttt caa ggg gtc tgg ccc cca ccg cat ttt tcg cat ttg		1315	
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<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

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Ile Thr Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser	
35 40 45	
Ala Val Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly	
50 55 60	
Ile Asp Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met	
65 70 75 80	
Glu Val Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val	
85 90 95	
Gly Ile Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser	
100 105 110	

Gly Ala His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu
 115 120 125
 Ile Arg Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg
 130 135 140
 Gly Thr Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu
 145 150 155 160
 Ala Asp Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp
 165 170 175
 Gln Val Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly
 180 185 190
 Leu Ile Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile
 195 200 205
 Ala Pro Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser
 210 215 220
 Asp Leu Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln
 225 230 235 240
 Leu Ala Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr
 245 250 255
 Asn Asp Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr
 260 265 270
 Pro Ile Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro
 275 280 285
 Pro Glu Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp
 290 295 300
 Arg Met Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp
 305 310 315 320
 Ser Gly Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr
 325 330 335
 Ile Asp Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu
 340 345 350
 Val Asp Ala Arg Pro Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser
 355 360 365
 Pro Arg Gln Cys Leu Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp
 370 375 380
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 385 390 395 400
 His Phe Ser His Leu Gly Ser
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<211> 351

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(328)

<223> RXN00617

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 Met Asp Glu Gln Glu
 1 5

gcc ctg ttc gat cgc ttc tcc aga ggc tcc caa aaa aat tca cgg cgt 163
 Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln Lys Asn Ser Arg Arg
 10 15 20

ccc ggt ggc gct ggc ctg gga tta tcc att gtc aag gcg atc ggc gaa 211
 Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val Lys Ala Ile Gly Glu
 25 30 35

gcc cac gtc ggc cga gct ttc gtc aat tcc aca cca ggt cta gga tcc 259
 Ala His Val Gly Arg Ala Phe Val Asn Ser Thr Pro Gly Leu Gly Ser
 40 45 50

att ttc ggc ctg gaa atc ccc gca cca gaa caa tca aag gaa tac acc 307
 Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln Ser Lys Glu Tyr Thr
 55 60 65

cat gag caa gat cct gct cgc tgaagatgac gccggcatcg cag 351
 His Glu Gln Asp Pro Ala Arg
 70 75

<210> 248

<211> 76

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

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Lys Asn Ser Arg Arg Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val
 20 25 30

Lys Ala Ile Gly Glu Ala His Val Gly Arg Ala Phe Val Asn Ser Thr
 35 40 45

Pro Gly Leu Gly Ser Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln
 50 55 60

Ser Lys Glu Tyr Thr His Glu Gln Asp Pro Ala Arg
 65 70 75

<210> 249

<211> 720

<212> DNA

<223> RXN02990

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185 190 195

aaa aac taaaccccg atgggaatca tcc
Lys Asn

720

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<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
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Asn Phe Glu Arg Ala His Ala Arg Gly Glu Ser Asp Phe Phe Asp His
20 25 30
Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu
35 40 45
Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys
50 55 60
Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu
65 70 75 80
Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val
85 90 95
Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg
100 105 110
Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu
115 120 125
Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
130 135 140
Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
145 150 155 160
Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
165 170 175
Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
180 185 190
Arg Ile Glu Asp Leu Lys Asn
195

<210> 251
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(318)
<223> RXN03100

<400> 251

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 1 5 10 15

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 Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
 20 25 30

gat gtc gcc gca att caa gca gcc gcc gac gga acc act ttt gat gca 144
 Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
 35 40 45

cca gaa gga acc gtg gtg gtt ggc ggc gat aac cac cac atc tcc aaa 192
 Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
 50 55 60

aca ccg cgc atc ggt cga atc cgc ccg gat gga ttg atc gac acc att 240
 Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
 65 70 75 80

tgg gaa acc gat tcc cca gtt gat ccg gac cca tac ttg tct tcc tat 288
 Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
 85 90 95

gac tgg gcc aag acc acc gct gcg act tcc taagagataa aaatcatgga cat 341
 Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
 100 105

<210> 252

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 252

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 20 25 30

Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
 35 40 45

Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
 50 55 60

Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
 65 70 75 80

Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
 85 90 95

Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
 100 105

<210> 253

<400> 254
Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
1 5 10 15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
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 Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
 35 40 45
 Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
 50 55 60
 Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
 65 70 75 80
 Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
 85 90 95
 Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
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 Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
 115 120 125
 Phe Val Ile Pro Arg Gly
 130

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 <212> DNA
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 Val Thr Glu Leu Ile
 1 5

 cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
 Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
 10 15 20

 gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
 25 30 35

 gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
 40 45 50

 cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
 55 60 65

 aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val

70	75					80					85					
acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg	Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val					90 95 100										403
gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat	Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His					105 110 115										451
gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc	Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg					120 125 130										499
att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt	Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg					135 140 145										547
ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg	Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val					150 155 160 165										595
ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct	Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala					170 175 180										643
gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt	Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly					185 190 195										691
ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg	Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr					200 205 210										739
ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag	Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys					215 220 225										787
gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc	Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu					230 235 240 245										835
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg	Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu					250 255 260										883
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct	Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro					265 270 275										931
ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc	Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr					280 285 290										979
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag	Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu					295 300 305										1027
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat	Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp					310 315 320 325										1075

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 1123
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
 330 335 340

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 1171
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
 345 350 355

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 1219
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
 360 365 370

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 1267
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
 375 380 385

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 1315
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
 390 395 400 405

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 1363
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
 410 415 420

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 1409
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 425 430

tttctcgacg ccc 1422

<210> 256
 <211> 433
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256
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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
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Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Th Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
 130 135 140
 Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
 145 150 155 160
 Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
 165 170 175
 Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
 180 185 190
 Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
 195 200 205
 Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
 210 215 220
 Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
 225 230 235 240
 Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
 245 250 255
 Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala
 260 265 270
 Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg
 275 280 285
 Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 290 295 300
 Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
 305 310 315 320
 Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
 325 330 335
 Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
 340 345 350
 Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
 355 360 365
 Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
 370 375 380
 Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
 385 390 395 400
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 405 410 415
 Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
 420 425 430

Ala

<400> 257																
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Met Ser Arg Ser Pro 1 5																
ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163																
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser 10 15 20																
cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211																
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly 25 30 35																
gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259																
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val 40 45 50																
tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307																
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr 55 60 65																
ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta 355																
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val 70 75 80 85																
gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca 403																
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala 90 95 100																
acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg 451																
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala 105 110 115																
atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa 499																
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu 120 125 130																
att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg 547																
Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val 135 140 145																
aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg 595																
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu 150 155 160 165																
ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc 643																
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly 170 175 180																

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa 691
 Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
 185 190 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg 738
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<210> 258

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

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Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
 20 25 30

Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
 35 40 45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr
 50 55 60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu
 65 70 75 80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala
 85 90 95

Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro
 100 105 110

Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr
 115 120 125

Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg
 130 135 140

Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg
 145 150 155 160

Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val
 165 170 175

Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala
 180 185 190

Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu
 195 200 205

<210> 259

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> RXN01349

<400> 259

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                                         Met Ala Thr Ser Arg
                                         1 5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct 163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
                        10 15 20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg 211
Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val Val Ala Thr Ala Leu
                        25 30 35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc 259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
                        40 45 50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc 307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
                        55 60 65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg 355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
                        70 75 80 85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt 403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val
                        90 95 100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag 451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
                        105 110 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa 499
His Pro Glu Ala Val Arg Leu Leu Met Glu Asn Leu His Ser Gln
                        120 125 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg 547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
                        135 140 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc gcc gcc ttc 595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
                        150 155 160 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg 643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
                        170 175 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc 691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
                        185 190 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc 739

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Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
 200 205 210
 gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc 787
 Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
 215 220 225
 aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act 835
 Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
 230 235 240 245
 gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac 877
 Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
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<210> 260
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 260
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 Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val
 20 25 30
 Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
 35 40 45
 Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
 50 55 60
 His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser
 65 70 75 80
 Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp
 85 90 95
 Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr
 100 105 110
 Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu
 115 120 125
 Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp
 130 135 140
 Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln
 145 150 155 160
 Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val
 165 170 175
 Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu
 180 185 190
 Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly

195	200	205
Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn		
210	215	220
Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr		
225	230	235
Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val		
	245	250
		255
Phe Glu Asn		

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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(769)
 <223> RXN00467

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 Met His Ile Ser Asp
 1 5
 ctt ccc gat agg tcc cag gac tac ctg aag aca atc tgg gac atc aca 163
 Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr Ile Trp Asp Ile Thr
 10 15 20
 gaa ctc ctt gat gat caa cca gca gca ctc ggc gat atc gcc gaa aaa 211
 Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly Asp Ile Ala Glu Lys
 25 30 35
 atg aac cag aaa act cct acc gcc tcc gaa gca atc aaa aag ctg gcg 259
 Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala Ile Lys Lys Leu Ala
 40 45 50
 gca agg ggc ctg gtc aac cat gaa aaa tat gct ggt gtc acc ctc act 307
 Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala Gly Val Thr Leu Thr
 55 60 65
 gaa cag ggc aaa acg cta gcc atc gac atg gtg cga cgc cac cgc ctg 355
 Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val Arg Arg His Arg Leu
 70 75 80 85
 ctg gaa acc ttc ctc cac gat gtt ttg gga tac acc tgg gac gaa gtc 403
 Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr Thr Trp Asp Glu Val
 90 95 100
 cac gcc gat gca gac ctg ttg gaa cat gca gcc tct gat cag ctc atc 451
 His Ala Asp Ala Asp Leu Leu Glu His Ala Ala Ser Asp Gln Leu Ile
 105 110 115
 gaa cgc atc gat gct cac ttg ggt cgt cca cgc aaa gat ccc cac ggc 499

Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg Lys Asp Pro His Gly
 120 125 130
 gat ccc ata cca act gcc gaa ggc gtt att gaa gag tct ccc cga acc 547
 Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu Glu Ser Pro Arg Thr
 135 140 145
 acc ctc gag gca gtt cag cca ggg gag act gtc acg att tcc agg gtc 595
 Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val Thr Ile Ser Arg Val
 150 155 160 165
 aaa gac att gat cct gaa ttg ctg cgc tac ctc gcg caa tac aac gtc 643
 Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu Ala Gln Tyr Asn Val
 170 175 180
 tca cca gga tgc cgg atc acc gtt gcg tcc ggc cca cta gct ggc atg 691
 Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly Pro Leu Ala Gly Met
 185 190 195
 gtg cat gtc gtt gta gaa ggc acc gac acc agc ttc ccc ctg gcc gaa 739
 Val His Val Val Val Glu Gly Thr Asp Thr Ser Phe Pro Leu Ala Glu
 200 205 210
 acg caa ctg cca tta att aca gtg cag gac taagcagatt catcataatg gtg 792
 Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
 215 220

<210> 262

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met His Ile Ser Asp Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr
 1 5 10 15
 Ile Trp Asp Ile Thr Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly
 20 25 30
 Asp Ile Ala Glu Lys Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala
 35 40 45
 Ile Lys Lys Leu Ala Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala
 50 55 60
 Gly Val Thr Leu Thr Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val
 65 70 75 80
 Arg Arg His Arg Leu Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr
 85 90 95
 Thr Trp Asp Glu Val His Ala Asp Ala Asp Leu Leu Glu His Ala Ala
 100 105 110
 Ser Asp Gln Leu Ile Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg
 115 120 125
 Lys Asp Pro His Gly Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu
 130 135 140

Glu Ser Pro Arg Thr Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val
 145 150 155 160
 Thr Ile Ser Arg Val Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu
 165 170 175
 Ala Gln Tyr Asn Val Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly
 180 185 190
 Pro Leu Ala Gly Met Val His Val Val Val Glu Gly Thr Asp Thr Ser
 195 200 205
 Phe Pro Leu Ala Glu Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
 210 215 220

<210> 263
 <211> 861
 <212> DNA
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<220>
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 <222> (101)..(838)
 <223> RXN02954

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 aagcttcata tcacttttcc acagcctgaa agaacatact atg tcc gca gct tta 115
 Met Ser Ala Ala Leu
 1 5
 cct cac aca gca gca gat ccc gta cac acc acc cca gcg aaa ccg ctg 163
 Pro His Thr Ala Ala Asp Pro Val His Thr Thr Pro Ala Lys Pro Leu
 10 15 20
 ctc gat cat gtc tta gat tca cta gga cgc agc atc atc agt ggt gaa 211
 Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser Ile Ile Ser Gly Glu
 25 30 35
 atg gaa gcc ggt agc aca ttc aaa ctg caa gac atc ggt gaa aaa ttc 259
 Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp Ile Gly Glu Lys Phe
 40 45 50
 ggt atc tcc cgc acc gtc gcc aga gaa gcc atg cgt gcc tta gag caa 307
 Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu Glu Gln
 55 60 65
 ctt ggg ttg gtg gcc tca tcg aga cga att ggt att aca gtg ctc tcg 355
 Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val Leu Ser
 70 75 80 85
 cac gag cac tgg gct gtc ttt gac aaa gcc att att cgc tgg cgc ctc 403
 His Glu His Trp Ala Val Phe Asp Lys Ala Ile Ile Arg Trp Arg Leu
 90 95 100
 gaa gat gag cgt caa cgt gaa cag caa ctg cag tca ctc acc gaa ctt 451
 Glu Asp Glu Arg Gln Arg Glu Gln Leu Gln Ser Leu Thr Glu Leu
 105 110 115

cgt att gcc att gaa cca att gct gca cgc agt gtt gcc ctt cat gca 499
 Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu His Ala
 120 125 130
 tcg agc gca gag att gct atc atc ggt gat ctt gct gca cga atg cgt 547
 Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu Ala Ala Arg Met Arg
 135 140 145
 aac ctc ggt gaa gct ggt cgt ggc gca tca caa gaa ttc cta gac gca 595
 Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln Glu Phe Leu Asp Ala
 150 155 160 165
 gat gtg aaa ttt cat gag ctt att ttg cag tat tgc cat aat gag atg 643
 Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr Cys His Asn Glu Met
 170 175 180
 ttc gct gcc atg gca cca ccc ata aaa gct gta cta gtc ggg cgc acc 691
 Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val Leu Val Gly Arg Thr
 185 190 195
 aca ctt ggc ctt caa ccc gat cga cct gcc gaa gaa gtc ttg gac aat 739
 Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu Glu Val Leu Asp Asn
 200 205 210
 cat gat gct ctc gca cac gca cta agt gtt cgt aat gca gac ctc gcc 787
 His Asp Ala Leu Ala His Ala Leu Ser Val Arg Asn Ala Asp Leu Ala
 215 220 225
 gaa aaa gca tcc agg agc att ctg aat gag gtg cgc gac gca ctg acc 835
 Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val Arg Asp Ala Leu Thr
 230 235 240 245
 tcg taattgccac taaacgagtc act 861
 Ser

<210> 264
 <211> 246
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
 Met Ser Ala Ala Leu Pro His Thr Ala Ala Asp Pro Val His Thr Thr
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 Pro Ala Lys Pro Leu Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser
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 Ile Ile Ser Gly Glu Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp
 35 40 45
 Ile Gly Glu Lys Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met
 50 55 60
 Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly
 65 70 75 80
 Ile Thr Val Leu Ser His Glu His Trp Ala Val Phe Asp Lys Ala Ile
 85 90 95

Ile Arg Trp Arg Leu Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln
 100 105 110
 Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser
 115 120 125
 Val Ala Leu His Ala Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu
 130 135 140
 Ala Ala Arg Met Arg Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln
 145 150 155 160
 Glu Phe Leu Asp Ala Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr
 165 170 175
 Cys His Asn Glu Met Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val
 180 185 190
 Leu Val Gly Arg Thr Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu
 195 200 205
 Glu Val Leu Asp Asn His Asp Ala Leu Ala His Ala Leu Ser Val Arg
 210 215 220
 Asn Ala Asp Leu Ala Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val
 225 230 235 240
 Arg Asp Ala Leu Thr Ser
 245

<210> 265
 <211> 480
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(457)
 <223> RXN03023

<400> 265
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 ttagttatat gagtaaccaa ccatcgggat cgtcgcgacc gtg cct ctg tat aaa 115
 Val Pro Leu Tyr Lys
 1 5
 cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163
 Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser
 10 15 20
 att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211
 Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg
 25 30 35
 att aat ccc gcc acc gca cgc aac ggc ctg acc ctc ctt gtc gaa gcc 259
 Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala
 40 45 50

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ggc atc ctc tat aag aag cgt ggc att ggc atg ttc gtc agc gcc cag 307
Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln
   55                                60                                65

gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355
Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
   70                                75                                80                                85

tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
                   90                                95                                100

gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg ggc ctg 451
Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
                   105                                110                                115

tac aag tagcgcttaa accctcttga cct 480
Tyr Lys

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<210> 266
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

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<400> 266
Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
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Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
   20                                25                                30

Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
   35                                40                                45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
   50                                55                                60

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
   65                                70                                75                                80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
   85                                90                                95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
  100                                105                                110

Glu Ser Arg Gly Leu Tyr Lys
  115

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<210> 267
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXN03127

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<400> 267

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gatatgatca gaaccatctc cagattagga agtgaacaca atg gaa agc tcc aaa 115
                                         Met Glu Ser Ser Lys
                                         1      5

aag act tcg cga tca agg tcc act act caa gaa gca gtg cgc gac att 163
Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu Ala Val Arg Asp Ile
              10              15              20

aaa aaa tac att cgg gac aac cgg ctg cgt acg gga gac ctt ctt cct 211
Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr Gly Asp Leu Leu Pro
              25              30              35

tcc gaa gcg ttc tta tgt gag gaa ttg ggt tgt tcc cgt tct gcg atc 259
Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys Ser Arg Ser Ala Ile
              40              45              50

agg gag gcg atc cgc gcg ctc gtg acc ttg gac atc gtc gag gtt cgc 307
Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp Ile Val Glu Val Arg
              55              60              65

cac ggc tac ggc act ttc gtg tcc agg atg tcc ctc gag ccc ctg atc 355
His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser Leu Glu Pro Leu Ile
              70              75              80              85

aac ggg atg gtg ttc cgc acg gtg ttg gac aat gac acc tcg gtg gaa 403
Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn Asp Thr Ser Val Glu
              90              95              100

aac ctt ttc tac gtg gtg gat acc cgc gaa atc ctt gac ctt tca ctt 451
Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile Leu Asp Leu Ser Leu
              105              110              115

ggc gaa gag ctg atc gag gtg ttc acc gac gat gac cgc gag cta ctc 499
Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp Asp Arg Glu Leu Leu
              120              125              130

ctt gat ctg gtg gac aag atg cgc gag cac aac gat cag ggc gaa tcc 547
Leu Asp Leu Val Asp Lys Met Arg Glu His Asn Asp Gln Gly Glu Ser
              135              140              145

ttt gtg gtg gag gat caa aaa ttc cac cga gca ctc cta gcg cga acg 595
Phe Val Val Glu Asp Gln Lys Phe His Arg Ala Leu Leu Ala Arg Thr
              150              155              160              165

aaa aac ccg ctg att aga gag ctc aac gat gcg ttt tgg cag atc caa 643
Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala Phe Trp Gln Ile Gln
              170              175              180

acc gag gcg cag ccc atg ctc aat ctg gct atg ccc gca gac atc gac 691
Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met Pro Ala Asp Ile Asp
              185              190              195

gaa acc atc aaa gct cac agc gac atc gtc gaa gcg ctc tcc agc ggc 739
Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu Ala Leu Ser Ser Gly
              200              205              210

aac atc gac gat tat cgc agc gcc gtg ctc gct cac tac gcg ccg ttt 787

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Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala His Tyr Ala Pro Phe
 215 220 225

cgc cgc atg att tcc aac atg ctc gat gcg cac tagcctcatt gcgcgcgggt 840
 Arg Arg Met Ile Ser Asn Met Leu Asp Ala His
 230 235 240

tgt 843

<210> 268

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Glu Ser Ser Lys Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu
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Ala Val Arg Asp Ile Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr
 20 25 30

Gly Asp Leu Leu Pro Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys
 35 40 45

Ser Arg Ser Ala Ile Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp
 50 55 60

Ile Val Glu Val Arg His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser
 65 70 75 80

Leu Glu Pro Leu Ile Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn
 85 90 95

Asp Thr Ser Val Glu Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile
 100 105 110

Leu Asp Leu Ser Leu Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp
 115 120 125

Asp Arg Glu Leu Leu Leu Asp Leu Val Asp Lys Met Arg Glu His Asn
 130 135 140

Asp Gln Gly Glu Ser Phe Val Val Glu Asp Gln Lys Phe His Arg Ala
 145 150 155 160

Leu Leu Ala Arg Thr Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala
 165 170 175

Phe Trp Gln Ile Gln Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met
 180 185 190

Pro Ala Asp Ile Asp Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu
 195 200 205

Ala Leu Ser Ser Gly Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala
 210 215 220

His Tyr Ala Pro Phe Arg Arg Met Ile Ser Asn Met Leu Asp Ala His
 225 230 235 240

<210> 269
 <211> 1691
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1668)
 <223> RXN03155

<400> 269
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 Gly Tyr Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
 1 5 10 15
 cca caa ctg atc aga gag ctt ctc gac gcg acc ccc atc gat cat tgg 96
 Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
 20 25 30
 tcc aac gat cgg cct act ctc acg ctg cca gag cat tgg gtg aca gac 144
 Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
 35 40 45
 atc gac att aag aac cct gtg ctt cgg gaa gtc gcc tcc cat ccc ttc 192
 Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
 50 55 60
 ttc gat ggc tgc ccg atc gga gat tta gat gcc gat gcc ttt gtg gag 240
 Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
 65 70 75 80
 gat ggc acc ctc att cac gaa aac ggg act tta aga ttc cgc agc cct 288
 Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
 85 90 95
 gag gaa cgc acc ttg gtt cgg gct tct act ccc cca tcg atg gca aga 336
 Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg
 100 105 110
 agc ccg ccg gag tgg gaa tcg acg gag gga ggc gtc gat aag cta att 384
 Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile
 115 120 125
 gcc gca gga aac ctg ccc ctg gcc cga ctg cat gta gag gaa cta ccc 432
 Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro
 130 135 140
 cgt gcc gat gag cag cgc gca ttt ttg gcg ctg tac ggc ggg cag tcg 480
 Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser
 145 150 155 160
 ttt gag gcg gcc tcg gcg tcg ccg ttt tat gcg ctg gcc acc tgg aat 528
 Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn
 165 170 175
 ccg gag gcg ttg ccg ggc gat ccg acc ttc gat atg ttc gcc gat gcg 576
 Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala

180						185						190						
cta	gac	act	ggg	cat	tac	agg	gaa	gtc	ccg	cgt	ccg	gat	gcc	cct	gaa			624
Leu	Asp	Thr	Gly	His	Tyr	Arg	Glu	Val	Pro	Arg	Pro	Asp	Ala	Pro	Glu			
		195					200					205						
gaa	agc	cag	atc	cac	gat	ttc	atc	agt	ggc	tgg	ctg	gcg	ttg	gtt	tac			672
Glu	Ser	Gln	Ile	His	Asp	Phe	Ile	Ser	Gly	Trp	Leu	Ala	Leu	Val	Tyr			
	210					215					220							
gat	gat	ccc	ctc	acc	gcc	cgc	cgt	ctg	ctc	tcc	agt	agg	ggc	ccc	tcc			720
Asp	Asp	Pro	Leu	Thr	Ala	Arg	Arg	Leu	Leu	Ser	Ser	Arg	Gly	Pro	Ser			
225					230					235					240			
gat	ttg	gtg	gga	ctg	tgg	cag	tcg	gcg	ttt	ttg	gcg	cga	gcg	cac	tac			768
Asp	Leu	Val	Gly	Leu	Trp	Gln	Ser	Ala	Phe	Leu	Ala	Arg	Ala	His	Tyr			
				245					250					255				
gtg	ctg	gga	gaa	ttc	caa	gaa	gcc	tcc	gcc	gtt	gtc	gaa	cgc	ggc	cta			816
Val	Leu	Gly	Glu	Phe	Gln	Glu	Ala	Ser	Ala	Val	Val	Glu	Arg	Gly	Leu			
			260					265					270					
gcc	acc	ggc	gac	cgc	acc	gga	gcc	tcc	cta	ctc	gaa	ccc	gtg	cac	ctg			864
Ala	Thr	Gly	Asp	Arg	Thr	Gly	Ala	Ser	Leu	Leu	Glu	Pro	Val	His	Leu			
		275					280					285						
tgg	acc	ggc	gcc	caa	gtc	gca	gcc	atg	act	ggg	cgc	acc	gaa	ttg	gcc			912
Trp	Thr	Gly	Ala	Gln	Val	Ala	Ala	Met	Thr	Gly	Arg	Thr	Glu	Leu	Ala			
	290					295					300							
aac	cac	tat	tta	cag	cgc	ctg	acc	gtg	ccc	gac	gat	gcg	ttc	ctc	atc			960
Asn	His	Tyr	Leu	Gln	Arg	Leu	Thr	Val	Pro	Asp	Asp	Ala	Phe	Leu	Ile			
305					310					315					320			
caa	aaa	ctc	agc	gca	tcc	atg	ggc	aaa	ttg	atc	acc	gca	tcc	atg	acc			1008
Gln	Lys	Leu	Ser	Ala	Ser	Met	Gly	Lys	Leu	Ile	Thr	Ala	Ser	Met	Thr			
				325					330					335				
tca	gac	acc	cgc	gca	gca	acc	ttg	gcc	ggc	gac	cgc	atg	gcg	tcg	gtc			1056
Ser	Asp	Thr	Arg	Ala	Ala	Thr	Leu	Ala	Gly	Asp	Arg	Met	Ala	Ser	Val			
			340					345					350					
gta	tac	acc	acc	aat	acc	cag	cag	ccc	gga	ttt	tgg	gcc	tgg	gaa	gac			1104
Val	Tyr	Thr	Thr	Asn	Thr	Gln	Gln	Pro	Gly	Phe	Trp	Ala	Trp	Glu	Asp			
		355					360					365						
atg	tat	gcg	atc	tca	ttg	atc	cga	acg	gga	cgc	atc	gac	gcc	gca	gcc			1152
Met	Tyr	Ala	Ile	Ser	Leu	Ile	Arg	Thr	Gly	Arg	Ile	Asp	Ala	Ala	Ala			
	370					375					380							
gcc	gtc	atg	gat	ggc	atc	cct	gac	tcc	acc	atc	ccc	tcg	ctg	cgt	gcc			1200
Ala	Val	Met	Asp	Gly	Ile	Pro	Asp	Ser	Thr	Ile	Pro	Ser	Leu	Arg	Ala			
385					390					395					400			
cga	aat	ttg	gtg	ccc	caa	gca	aac	atc	gaa	atc	caa	cga	ggc	tcc	aca			1248
Arg	Asn	Leu	Val	Pro	Gln	Ala	Asn	Ile	Glu	Ile	Gln	Arg	Gly	Ser	Thr			
				405					410					415				
gca	cga	ggc	gta	aaa	atg	ctc	tcc	gaa	gcc	gtc	gac	ctc	att	tcc	tcc			1296
Ala	Arg	Gly	Val	Lys	Met	Leu	Ser	Glu	Ala	Val	Asp	Leu	Ile	Ser	Ser			
			420					425					430					

gtc aac atg cca gca tat gaa gcc cgc atc ctc ttc gaa tac ggg ctg 1344
 Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu
 435 440 445
 gtt cta cga cgc atg ggc agg cgc agc caa gca gcc gaa atg ttc acc 1392
 Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr
 450 455 460
 cac gcc gaa gaa gtc ttc acc gcc atg ggt gcg gtc act ctg gct gcc 1440
 His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala
 465 470 475 480
 cgc tgc cac ggc gaa cga cga gtc gca ggc gtt ggg cca cgc aga tca 1488
 Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser
 485 490 495
 gcg cag gga ctc acc cct caa gag gaa caa atc act gcg ctg gtt gtc 1536
 Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val
 500 505 510
 gac ggc tgc tcc aac caa gaa gtc gcc cgt gag ctt tcc ctc tcc gcc 1584
 Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala
 515 520 525
 aaa acg gtg gaa tat cac ctc acg agg gtg tac aaa aag ctc ggg gtg 1632
 Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val
 530 535 540
 agc tcc cgt gga gag ctt cga gaa tta ctg aag gtc tgacacagcg 1678
 Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
 545 550 555
 ttgttcagca gct 1691

<210> 270

<211> 556

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Gly Tyr Pro Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
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Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
 20 25 30

Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
 35 40 45

Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
 50 55 60

Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
 65 70 75 80

Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
 85 90 95

Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg

100					105					110					
Ser	Pro	Arg	Glu	Trp	Glu	Ser	Thr	Glu	Gly	Gly	Val	Asp	Lys	Leu	Ile
		115					120					125			
Ala	Ala	Gly	Asn	Leu	Pro	Leu	Ala	Arg	Leu	His	Val	Glu	Glu	Leu	Pro
		130				135					140				
Arg	Ala	Asp	Glu	Gln	Arg	Ala	Phe	Leu	Ala	Leu	Tyr	Gly	Gly	Gln	Ser
145					150					155					160
Phe	Glu	Ala	Ala	Ser	Ala	Ser	Pro	Phe	Tyr	Ala	Leu	Ala	Thr	Trp	Asn
				165					170					175	
Pro	Glu	Ala	Leu	Arg	Gly	Asp	Pro	Thr	Phe	Asp	Met	Phe	Ala	Asp	Ala
			180					185					190		
Leu	Asp	Thr	Gly	His	Tyr	Arg	Glu	Val	Pro	Arg	Pro	Asp	Ala	Pro	Glu
		195					200					205			
Glu	Ser	Gln	Ile	His	Asp	Phe	Ile	Ser	Gly	Trp	Leu	Ala	Leu	Val	Tyr
		210					215				220				
Asp	Asp	Pro	Leu	Thr	Ala	Arg	Arg	Leu	Leu	Ser	Ser	Arg	Gly	Pro	Ser
225					230					235					240
Asp	Leu	Val	Gly	Leu	Trp	Gln	Ser	Ala	Phe	Leu	Ala	Arg	Ala	His	Tyr
				245					250					255	
Val	Leu	Gly	Glu	Phe	Gln	Glu	Ala	Ser	Ala	Val	Val	Glu	Arg	Gly	Leu
			260					265					270		
Ala	Thr	Gly	Asp	Arg	Thr	Gly	Ala	Ser	Leu	Leu	Glu	Pro	Val	His	Leu
		275					280					285			
Trp	Thr	Gly	Ala	Gln	Val	Ala	Ala	Met	Thr	Gly	Arg	Thr	Glu	Leu	Ala
		290				295					300				
Asn	His	Tyr	Leu	Gln	Arg	Leu	Thr	Val	Pro	Asp	Asp	Ala	Phe	Leu	Ile
305					310					315					320
Gln	Lys	Leu	Ser	Ala	Ser	Met	Gly	Lys	Leu	Ile	Thr	Ala	Ser	Met	Thr
				325					330					335	
Ser	Asp	Thr	Arg	Ala	Ala	Thr	Leu	Ala	Gly	Asp	Arg	Met	Ala	Ser	Val
			340					345					350		
Val	Tyr	Thr	Thr	Asn	Thr	Gln	Gln	Pro	Gly	Phe	Trp	Ala	Trp	Glu	Asp
			355				360					365			
Met	Tyr	Ala	Ile	Ser	Leu	Ile	Arg	Thr	Gly	Arg	Ile	Asp	Ala	Ala	Ala
		370				375					380				
Ala	Val	Met	Asp	Gly	Ile	Pro	Asp	Ser	Thr	Ile	Pro	Ser	Leu	Arg	Ala
385					390					395					400
Arg	Asn	Leu	Val	Pro	Gln	Ala	Asn	Ile	Glu	Ile	Gln	Arg	Gly	Ser	Thr
				405					410					415	
Ala	Arg	Gly	Val	Lys	Met	Leu	Ser	Glu	Ala	Val	Asp	Leu	Ile	Ser	Ser
			420					425					430		

Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu
435 440 445

Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr
450 455 460

His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala
465 470 475 480

Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser
485 490 495

Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val
500 505 510

Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala
515 520 525

Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val
530 535 540

Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
545 550 555

<210> 271

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXN01315

<400> 271

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aatattgcac tgagtgcgaag ttacactag gtttacttca gtg gat att gaa gag 115
Val Asp Ile Glu Glu
1 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
55 60 65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His

70	75	80	85	
gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc				403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly				
	90	95	100	
aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga				451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg				
	105	110	115	
cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc				499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe				
	120	125	130	
gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag				547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu				
	135	140	145	
tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat				595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp				
	150	155	160	165
cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa				643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln				
	170	175	180	
ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc				691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe				
	185	190	195	
caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt				739
Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly				
	200	205	210	
gga ttt tca gaa tgacatcaca ggtcaagccg gac				774
Gly Phe Ser Glu				
	215			

<210> 272

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met	
1 5 10 15	

Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg	
20 25 30	

Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile	
35 40 45	

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala	
50 55 60	

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe	
65 70 75 80	

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val	
---	--

85										90					95				
Ile	Asn	Leu	Phe	Gly	Asn	His	Asp	Asn	Ser	Lys	Ser	Gly	Val	Ala	Gly				
			100					105					110						
Asp	Ile	Met	Arg	Arg	Arg	Lys	Glu	Ile	Arg	Val	Lys	His	Pro	Glu	Leu				
		115					120					125							
Ala	Val	Gln	His	Phe	Ala	Arg	Phe	His	Gln	Ala	Arg	Glu	Gly	Leu	Glu				
		130				135					140								
His	Leu	Ile	Val	Glu	Tyr	Phe	Glu	Lys	Trp	Pro	Gly	Ser	Gln	His	Leu				
145					150					155					160				
Asp	Glu	Pro	Ala	Asp	Arg	Glu	Ala	Ile	Ala	Ile	Val	Gly	Leu	Leu	Ile				
				165					170					175					
Ser	Val	Met	Leu	Gln	Gly	Ser	Arg	Glu	Trp	His	Asp	Met	Pro	Gln	Gly				
			180					185					190						
Thr	Gln	Ala	Asp	Phe	Gln	Ala	Cys	Cys	Arg	Lys	Ala	Ile	Lys	Asn	Thr				
		195					200					205							
Phe	Leu	Leu	Arg	Gly	Gly	Phe	Ser	Glu											
	210					215													

<210> 273

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(457)

<223> RXN00035

<400> 273

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				Val	Pro	Leu	Tyr	Lys		
				1				5		

cag	atc	gct	tct	ttg	att	gag	gac	tcc	atc	gtt	gac	gga	acc	ttg	agc		163
Gln	Ile	Ala	Ser	Leu	Ile	Glu	Asp	Ser	Ile	Val	Asp	Gly	Thr	Leu	Ser		
			10					15						20			

att	gat	caa	cgc	gtg	cct	tct	act	aat	gaa	cta	gcc	gcg	ttc	cat	cgc		211
Ile	Asp	Gln	Arg	Val	Pro	Ser	Thr	Asn	Glu	Leu	Ala	Ala	Phe	His	Arg		
			25					30					35				

att	aat	ccc	gcc	acc	gca	cgc	aac	ggc	ctg	acc	ctc	ctt	gtc	gaa	gcc		259
Ile	Asn	Pro	Ala	Thr	Ala	Arg	Asn	Gly	Leu	Thr	Leu	Leu	Val	Glu	Ala		
		40					45					50					

ggc	atc	ctc	tat	aag	aag	cgt	ggc	att	ggc	atg	ttc	gtc	agc	gcc	cag		307
Gly	Ile	Leu	Tyr	Lys	Lys	Arg	Gly	Ile	Gly	Met	Phe	Val	Ser	Ala	Gln		
	55					60					65						

gcc	cca	gca	ctc	atc	cga	gag	cgg	cga	gat	gcc	gcc	ttc	gcg	gct	act		355
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Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
 70 75 80 85
 tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
 Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
 90 95 100
 gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg ggc ctg 451
 Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
 105 110 115
 tac aag tagcgccttaa accctcttga cct 480
 Tyr Lys

<210> 274
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 274
 Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
 1 5 10 15
 Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
 20 25 30
 Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
 35 40 45
 Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
 50 55 60
 Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
 65 70 75 80
 Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
 85 90 95
 Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
 100 105 110
 Glu Ser Arg Gly Leu Tyr Lys
 115

<210> 275
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 <212> DNA
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<220>
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 <222> (101)..(787)
 <223> RXN00049

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 cttatatttta agtcaccgca gatcagctaa gggtttccct atg ccc acg cct tcg 115

Met Pro Thr Pro Ser
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<210> 276
 <211> 229
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 276
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 1 5 10 15
 Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg
 20 25 30
 Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
 35 40 45
 Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
 50 55 60
 Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65 70 75 80
 Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
 85 90 95
 Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
 100 105 110
 His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
 115 120 125
 Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro
 130 135 140
 Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr
 145 150 155 160
 Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile
 165 170 175
 Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp
 180 185 190
 Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln
 195 200 205
 Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser
 210 215 220
 Pro Val Lys Pro Gln
 225

<210> 277
 <211> 1032
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1009)

<223> RXN00486

<400> 277

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caactatagt taagtaatac tgaacaattt tggaggtgtc gtg ctc aat ctc aac 115
                                   Val Leu Asn Leu Asn
                                   1      5
cgc tta cac atc ctg cag gaa ttc cac cgc ctg gga acg att aca gca 163
Arg Leu His Ile Leu Gln Glu Phe His Arg Leu Gly Thr Ile Thr Ala
              10              15              20
gtg gcg gaa tcc atg aac tac agc cgc tct gcc atc tcc caa caa atg 211
Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala Ile Ser Gln Gln Met
              25              30              35
gcg ctg ctg gaa aaa gaa att ggt gtg aaa ctc ttt gaa aaa agc ggc 259
Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu Phe Glu Lys Ser Gly
              40              45              50
cga aac ctc tac ttc aca gaa caa ggc gaa gtg ttg gcc tca gaa aca 307
Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val Leu Ala Ser Glu Thr
              55              60              65
cat gcg atc atg gca gca gtc gac cat gcc cgc gca gcc gtt cta gat 355
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
              70              75              80              85
tcg ctg tct gaa gtg tcc gga acg ctg aaa gtc acc tcc ttc caa tcc 403
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
              90              95              100
ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa 451
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
              105              110              115
tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg 499
Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
              120              125              130
ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa 547
Leu Glu Glu Leu Arg Ala Arg Val Asp Val Ala Leu Gly Glu Glu
              135              140              145
tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc 595
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
              150              155              160              165
ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac 643
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
              170              175              180
tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat 691
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
              185              190              195
cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc 739
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
              200              205              210

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gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc 787
 Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
 215 220 225

 caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca 835
 Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
 230 235 240 245

 ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc 883
 Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
 250 255 260

 aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg 931
 Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
 265 270 275

 cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa 979
 His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
 280 285 290

 gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca gac 1032
 Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
 295 300

<210> 278
 <211> 303
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 278
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 Gly Thr Ile Thr Ala Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala
 20 25 30

 Ile Ser Gln Gln Met Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu
 35 40 45

 Phe Glu Lys Ser Gly Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val
 50 55 60

 Leu Ala Ser Glu Thr His Ala Ile Met Ala Ala Val Asp His Ala Arg
 65 70 75 80

 Ala Ala Val Leu Asp Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val
 85 90 95

 Thr Ser Phe Gln Ser Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala
 100 105 110

 Arg Leu Thr Glu Lys Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu
 115 120 125

 Glu Val Thr Ala Ala Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val
 130 135 140

 Ala Leu Gly Glu Glu Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser
 145 150 155 160

Ile His Arg Glu Val Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro
 165 170 175
 Ala Ser Gly Pro Tyr Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile
 180 185 190
 Pro Ile Ala Ile Asp Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His
 195 200 205
 Arg Leu Cys Arg Arg Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr
 210 215 220
 Ser Asp Pro Met Leu Gln Ala His Leu Val Arg Ser Gly Leu Ala Val
 225 230 235 240
 Thr Phe Ser Pro Thr Leu Leu Thr Pro Met Leu Glu Ser Val His Ile
 245 250 255
 Gln Pro Leu Pro Gly Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg
 260 265 270
 Glu Gly Arg Gln Gly His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu
 275 280 285
 Ala His Val Ala Lys Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
 290 295 300

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 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(850)
 <223> RXN01081

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 Met Thr Pro Ala Asn
 1 5
 gaa agt cct atg act aat cca tta ggt tct gcc ccc acc cca gcc aag 163
 Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala Pro Thr Pro Ala Lys
 10 15 20
 cca ctt ctt gac agt gtt ctt gat gag ctc ggt caa gat atc atc agt 211
 Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly Gln Asp Ile Ile Ser
 25 30 35
 ggc aag gtt gct gtc gga gat acc ttc aag ctg atg gac atc ggc gag 259
 Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu Met Asp Ile Gly Glu
 40 45 50
 cgt ttt ggc att tcc cgc aca gtg gca cgc gaa gcg atg cgc gct ttg 307
 Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu
 55 60 65

gag cag ctc ggt ctt gtc gct tct tca cgt cgc att ggc att act gtt 355
 Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val
 70 75 80 85
 ttg cca cag gaa gag tgg gct gtt ttt gat aag tcc atc att cgc tgg 403
 Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys Ser Ile Ile Arg Trp
 90 95 100
 cgt ctc aat gac gaa ggt cag cgt gaa ggc cag ctt cag tct ctt acc 451
 Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln Leu Gln Ser Leu Thr
 105 110 115
 gag ctt cgt att gct att gaa ccg att gcc gcg cgc agc gtt gct ctt 499
 Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu
 120 125 130
 cac gcg tca acc gcc gag ctc gag aaa atc cgc gcg ctc gca aca gag 547
 His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg Ala Leu Ala Thr Glu
 135 140 145
 atg cgt cag ttg ggt gaa tct ggt cag ggt gcg tcc cag cgc ttc ctc 595
 Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala Ser Gln Arg Phe Leu
 150 155 160 165
 gaa gcg gac gtc act ttc cac gag ctc atc ttg cgt tat tgc cac aat 643
 Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu Arg Tyr Cys His Asn
 170 175 180
 gag atg ttc gct gca ctg att ccg tcc att agc gcg gtt ctt gtc ggc 691
 Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser Ala Val Leu Val Gly
 185 190 195
 cgc acc gag ctc ggc ctg cag cct gat ctg ccg gcg cac gag gcg cta 739
 Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro Ala His Glu Ala Leu
 200 205 210
 gac aac cac gat aag ctt gcc gac gcc ctc ctt aac cgc gac gcc gac 787
 Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu Asn Arg Asp Ala Asp
 215 220 225
 gcc gca gaa act gcg tcc cga aac atc ctc aat gag gtg cgc agc gcg 835
 Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn Glu Val Arg Ser Ala
 230 235 240 245
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 Leu Gly Thr Leu Asn
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<210> 280

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Thr Pro Ala Asn Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala
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 20 25 30

Gln Asp Ile Ile Ser Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu
 35 40 45
 Met Asp Ile Gly Glu Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu
 50 55 60
 Ala Met Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg
 65 70 75 80
 Ile Gly Ile Thr Val Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys
 85 90 95
 Ser Ile Ile Arg Trp Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln
 100 105 110
 Leu Gln Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala
 115 120 125
 Arg Ser Val Ala Leu His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg
 130 135 140
 Ala Leu Ala Thr Glu Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala
 145 150 155 160
 Ser Gln Arg Phe Leu Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu
 165 170 175
 Arg Tyr Cys His Asn Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser
 180 185 190
 Ala Val Leu Val Gly Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro
 195 200 205
 Ala His Glu Ala Leu Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu
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 225 230 235 240
 Glu Val Arg Ser Ala Leu Gly Thr Leu Asn
 245 250

<210> 281
 <211> 998
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(975)
 <223> RXN01160

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 ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc 96
 Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg

20					25					30						
gat	ctt	ggc	caa	ccc	tcc	tcc	caa	atc	atg	gaa	gac	ctc	aac	aga	tta	144
Asp	Leu	Gly	Gln	Pro	Ser	Ser	Gln	Ile	Met	Glu	Asp	Leu	Asn	Arg	Leu	
		35					40					45				
tgg	atg	tgt	ggg	ctg	cca	gga	ctt	ctt	cca	ggg	gac	ttg	gtg	gag	ctt	192
Trp	Met	Cys	Gly	Leu	Pro	Gly	Leu	Leu	Pro	Gly	Asp	Leu	Val	Glu	Leu	
	50					55					60					
gat	cat	tcc	ttt	aag	gaa	gta	aaa	atc	cac	aat	gct	caa	ggc	atg	gat	240
Asp	His	Ser	Phe	Lys	Glu	Val	Lys	Ile	His	Asn	Ala	Gln	Gly	Met	Asp	
	65				70					75					80	
aaa	ccc	ttg	cgc	ctc	aca	cca	act	gaa	gcc	ggg	gtt	ttg	ctg	ctg	aca	288
Lys	Pro	Leu	Arg	Leu	Thr	Pro	Thr	Glu	Ala	Gly	Val	Leu	Leu	Leu	Thr	
				85					90					95		
ctt	gaa	tcc	ctg	gaa	tcc	ctc	ccc	ggg	att	gcg	aaa	cag	gaa	gcg	gtc	336
Leu	Glu	Ser	Leu	Glu	Ser	Leu	Pro	Gly	Ile	Ala	Lys	Gln	Glu	Ala	Val	
			100					105					110			
gta	tct	gct	gcg	aac	aag	cta	cgc	gcc	atc	atg	ggg	gag	tat	tcc	tcg	384
Val	Ser	Ala	Ala	Asn	Lys	Leu	Arg	Ala	Ile	Met	Gly	Glu	Tyr	Ser	Ser	
		115					120					125				
act	gtt	ttc	gac	tcc	act	gga	gaa	gac	ctc	gat	gct	gaa	gtt	cta	gag	432
Thr	Val	Phe	Asp	Ser	Thr	Gly	Glu	Asp	Leu	Asp	Ala	Glu	Val	Leu	Glu	
	130					135					140					
atc	atc	cgc	gac	gcc	atg	gat	tta	cac	cag	cag	gtc	agt	ttt	gaa	tac	480
Ile	Ile	Arg	Asp	Ala	Met	Asp	Leu	His	Gln	Gln	Val	Ser	Phe	Glu	Tyr	
	145				150					155					160	
cac	tcg	cac	aga	tca	gac	aac	acc	agc	ctg	agg	caa	gtc	agc	cct	gct	528
His	Ser	His	Arg	Ser	Asp	Asn	Thr	Ser	Leu	Arg	Gln	Val	Ser	Pro	Ala	
				165					170					175		
cat	atc	ttc	acc	cat	gaa	ggc	gaa	acc	tac	atc	aaa	gcc	tgg	gaa	gaa	576
His	Ile	Phe	Thr	His	Glu	Gly	Glu	Thr	Tyr	Ile	Lys	Ala	Trp	Glu	Glu	
			180					185					190			
gct	gtg	aac	caa	tgg	cgg	acg	ttt	agg	ctt	gat	cgc	atc	cga	agc	att	624
Ala	Val	Asn	Gln	Trp	Arg	Thr	Phe	Arg	Leu	Asp	Arg	Ile	Arg	Ser	Ile	
		195					200					205				
gtg	ctt	ctt	gac	agc	aaa	gca	gtg	cac	ccg	gcg	cga	ggg	gtt	tca	gta	672
Val	Leu	Leu	Asp	Ser	Lys	Ala	Val	His	Pro	Ala	Arg	Gly	Val	Ser	Val	
	210					215					220					
tcc	acg	gac	gat	cct	ttt	gag	ttc	gca	aaa	tct	tcc	gat	att	gcc	acg	720
Ser	Thr	Asp	Asp	Pro	Phe	Glu	Phe	Ala	Lys	Ser	Ser	Asp	Ile	Ala	Thr	
	225				230					235					240	
tta	ttg	ctg	cgt	gag	gac	gca	atg	tgg	tta	ggc	aat	tac	atg	gcc	atg	768
Leu	Leu	Leu	Arg	Glu	Asp	Ala	Met	Trp	Leu	Gly	Asn	Tyr	Met	Ala	Met	
				245					250					255		
gag	gtg	gat	gaa	acg	gtg	gaa	ccg	att	cgc	gat	agc	gac	gga	ttc	agc	816
Glu	Val	Asp	Glu	Thr	Val	Glu	Pro	Ile	Arg	Asp	Ser	Asp	Gly	Phe	Ser	
			260					265					270			

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga 864
 Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
 275 280 285
 ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat 912
 Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
 290 295 300
 ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat 960
 Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
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 gat cat cac gta gag taacacccaa gagtaagacg caa 998
 Asp His His Val Glu
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45
 Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
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 Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
 65 70 75 80
 Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
 85 90 95
 Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
 100 105 110
 Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
 115 120 125
 Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
 130 135 140
 Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
 145 150 155 160
 His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
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 His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
 180 185 190
 Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile

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Val	Leu	Leu	Asp	Ser	Lys	Ala	Val	His	Pro	Ala	Arg	Gly	Val	Ser	Val
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Ser	Thr	Asp	Asp	Pro	Phe	Glu	Phe	Ala	Lys	Ser	Ser	Asp	Ile	Ala	Thr
225					230					235					240
Leu	Leu	Leu	Arg	Glu	Asp	Ala	Met	Trp	Leu	Gly	Asn	Tyr	Met	Ala	Met
				245					250					255	
Glu	Val	Asp	Glu	Thr	Val	Glu	Pro	Ile	Arg	Asp	Ser	Asp	Gly	Phe	Ser
			260					265					270		
Trp	His	Thr	Val	His	Phe	Pro	Leu	Leu	Ser	Arg	Asp	Trp	Phe	Val	Arg
		275					280					285			
Phe	Ala	Ile	Gly	His	Ala	Glu	His	Leu	Lys	Val	Thr	Ser	Pro	Glu	Asp
	290					295					300				
Leu	Arg	Lys	Cys	Ile	Lys	Gln	Lys	Ala	Phe	Ser	Gly	Leu	Ser	Ala	Tyr
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Asp	His	His	Val	Glu											
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 Met Pro Ala Gly Ile
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 Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
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 gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag 211
 Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
 25 30 35
 ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
 Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
 40 45 50
 ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa 307
 Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
 55 60 65
 atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg 355

Met 70	Thr	Pro	Cys	Leu	Thr 75	Val	Thr	Thr	Leu	Val 80	Ser	Arg	Ala	Ser	Arg 85	
atc	agc	gat	cca	gca	gat	ttc	ttc	ggt	gaa	tac	atc	gga	gga	ctg	gga	403
Ile	Ser	Asp	Pro	Ala	Asp	Phe	Phe	Gly	Glu	Tyr	Ile	Gly	Gly	Leu	Gly	
				90					95					100		
ctt	agc	gca	gaa	cac	gca	gca	gtt	gtt	gaa	ggg	ttg	acc	gaa	aag	ctc	451
Leu	Ser	Ala	Glu	His	Ala	Ala	Val	Val	Glu	Gly	Leu	Thr	Glu	Lys	Leu	
			105					110					115			
ttc	gca	cag	gct	ggc	ctg	ctc	gtt	cct	gag	gga	att	gca	tct	cca	ttg	499
Phe	Ala	Gln	Ala	Gly	Leu	Leu	Val	Pro	Glu	Gly	Ile	Ala	Ser	Pro	Leu	
		120					125					130				
gag	ttg	tta	tcc	atc	cac	gca	ggc	att	agt	aac	cac	gaa	gtg	gcc	gca	547
Glu	Leu	Leu	Ser	Ile	His	Ala	Gly	Ile	Ser	Asn	His	Glu	Val	Ala	Ala	
	135					140						145				
gtg	ctg	acc	gaa	gtg	gaa	aac	ggc	acc	acc	gaa	tat	cca	ttc	atg	ttc	595
Val	Leu	Thr	Glu	Val	Glu	Asn	Gly	Thr	Thr	Glu	Tyr	Pro	Phe	Met	Phe	
	150				155					160					165	
gac	gct	gtc	ctg	cgc	cta	acc	cct	gag	tgg	gca	cag	acc	ctt	atc	ggc	643
Asp	Ala	Val	Leu	Arg	Leu	Thr	Pro	Glu	Trp	Ala	Gln	Thr	Leu	Ile	Gly	
				170					175					180		
gga	gtt	caa	gaa	ctc	att	gaa	ttt	gcc	acc	acc	cac	cga	act	tct	tgg	691
Gly	Val	Gln	Glu	Leu	Ile	Glu	Phe	Ala	Thr	Thr	His	Arg	Thr	Ser	Trp	
			185					190					195			
tca	gac	cgc	cag	cgc	gaa	tcc	tca	ctg	cca	gcc	atg	atc	gat	gag	atc	739
Ser	Asp	Arg	Gln	Arg	Glu	Ser	Ser	Leu	Pro	Ala	Met	Ile	Asp	Glu	Ile	
		200					205					210				
gtt	gtg	gcg	gaa	ctt	cgg	gaa	cgc	cca	gtt	ggt	act	gcc	gac	cgt	gaa	787
Val	Val	Ala	Glu	Leu	Arg	Glu	Arg	Pro	Val	Gly	Thr	Ala	Asp	Arg	Glu	
	215					220					225					
aac	tcc	gtt	ggt	gtg	gca	ctt	cgt	gag	ctt	cgc	cca	cgc	ctc	atc	ctg	835
Asn	Ser	Val	Gly	Val	Ala	Leu	Arg	Glu	Leu	Arg	Pro	Arg	Leu	Ile	Leu	
	230				235					240					245	
gat	gca	gaa	cgc	cgc	aaa	gtc	tgc	ctg	cgt	cta	cct	gaa	cag	cgc	gtc	883
Asp	Ala	Glu	Arg	Arg	Lys	Val	Cys	Leu	Arg	Leu	Pro	Glu	Gln	Arg	Val	
				250					255					260		
agc	gac	gat	gaa	atc	aac	tgg	cga	gtc	agc	cta	gaa	ggc	acc	acc	cgg	931
Ser	Asp	Asp	Glu	Ile	Asn	Trp	Arg	Val	Ser	Leu	Glu	Gly	Thr	Thr	Arg	
			265					270					275			
att	ttc	tcc	acc	cgc	cga	gca	tgg	ggc	gat	act	tct	gga	tac	tcc	gaa	979
Ile	Phe	Ser	Thr	Arg	Arg	Ala	Trp	Gly	Asp	Thr	Ser	Gly	Tyr	Ser	Glu	
		280					285					290				
gcc	ctc	gac	atc	act	gtc	gag	cgt	caa	atc	cgc	gaa	acc	acc	gtc	acc	1027
Ala	Leu	Asp	Ile	Thr	Val	Glu	Arg	Gln	Ile	Arg	Glu	Thr	Thr	Val	Thr	
	295					300					305					
gac	acc	tca	aac	caa	atc	acc	tgg	gtt	gtc	cca	gtc	gtg	gac	ttc	aac	1075
Asp	Thr	Ser	Asn	Gln	Ile	Thr	Trp	Val	Val	Pro	Val	Val	Asp	Phe	Asn	

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gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag	1123			
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys				
330	335	340		
gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca	1171			
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala				
345	350	355		
aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa	1219			
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln				
360	365	370		
ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc	1267			
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala				
375	380	385		
cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac	1315			
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp				
390	395	400	405	
cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac	1363			
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His				
410	415	420		
gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc	1411			
Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala				
425	430	435		
gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc	1459			
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser				
440	445	450		
atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag	1507			
Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu				
455	460	465		
cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc	1555			
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe				
470	475	480	485	
gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga	1603			
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg				
490	495	500		
ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc	1651			
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val				
505	510	515		
gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga	1699			
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg				
520	525	530		
atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc	1747			
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser				
535	540	545		
ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca	1795			
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala				
550	555	560	565	

acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa	1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln	
570 575 580	
atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg	1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu	
585 590 595	
acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca	1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro	
600 605 610	
cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat	1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp	
615 620 625	
gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg	2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu	
630 635 640 645	
cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc	2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala	
650 655 660	
agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc	2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser	
665 670 675	
atc gaa ttt gag tgg act gac cgc aag gtt gac cgt cgc gtt tcc gtg	2179
Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Arg Val Ser Val	
680 685 690	
acg att gct gtc att gac aaa act gag aac ttt act ggc atc acc atc	2227
Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile	
695 700 705	
gaa gat gga aag ctc gta ttc gaa gaa ctc gca gcc ggt cgc caa ctc	2275
Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu	
710 715 720 725	
gct gca tgg gtg tgg cca caa acc gca ccg tgg gta agc gca gtg gaa	2323
Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu	
730 735 740	
ctt gct gtc acc gga cca gag ctg gaa ctc cct gaa gtt ctc gtc ggc	2371
Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly	
745 750 755	
gca ggc aac ctg att gtt caa ctc cac acc gct gac cca ttc act acc	2419
Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr	
760 765 770	
tcc gtg acc cca ctg tca cca gga aaa gct gcg gtc acc gtt gag caa	2467
Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln	
775 780 785	
gaa ggc tac tac tca gca caa acc gaa gaa tat gca cag ctt tca gca	2515
Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr Ala Gln Leu Ser Ala	
790 795 800 805	

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Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val	
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ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc	2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr	
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Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala	
840 845 850	
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Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro Ala Gln Ala Leu Pro	
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Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser Pro Phe Thr Thr Glu	
870 875 880 885	
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Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp Ile Gly Thr Leu Gln	
890 895 900	
ctc ctg ggt gca ctg cca agc gca ttc aag gaa gcc gaa gag ctt ggc	2851
Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu Ala Glu Glu Leu Gly	
905 910 915	
aac cgc aca cca ctg ctg cca atc ctc gga caa ctt gag gaa gtc gcc	2899
Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala	
920 925 930	
ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg	2947
Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu	
935 940 945	
gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac	2995
Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn	
950 955 960 965	
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970 975 980	
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Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val	
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Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg Glu Val Leu Gln Thr	
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Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu	
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Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro
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 Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu
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 1080 1085 1090
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 Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser
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 Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
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 Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
 65 70 75 80
 Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
 85 90 95
 Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
 100 105 110
 Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
 115 120 125
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 130 135 140
 His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
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 Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
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Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
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 His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
 195 200 205
 Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
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 Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
 225 230 235 240
 Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
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 Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
 260 265 270
 Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
 275 280 285
 Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
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 305 310 315 320
 Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
 325 330 335
 Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
 340 345 350
 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
 355 360 365
 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
 370 375 380
 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
 385 390 395 400
 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
 405 410 415
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
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 Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
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 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
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 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro

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Val	Thr	Val	Glu	Ala	Thr	Asp	Pro	Asn	Ala	Ser	Phe	Val	Val	Thr	Thr
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Asp	Glu	Gly	Asp	Gln	Met	Pro	Leu	Arg	Phe	Val	Pro	Pro	Gln	Ile	Ala
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Arg	Thr	Gly	Val	Asp	Val	Gly	Asp	Pro	Lys	Val	Ser	Val	Arg	Asn	His
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His	Gly	Ser	Pro	Leu	Arg	Thr	Val	Lys	Met	Val	Thr	Pro	Asp	Asn	Gly
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Met	Pro	Arg	Gly	Ser	Ile	Glu	Phe	Glu	Trp	Thr	Asp	Arg	Lys	Val	Asp
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Ala	Gln	Leu	Ser	Ala	Phe	Phe	Gly	Gly	Glu	Val	Glu	Glu	Pro	Pro	Ile
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Ser	Asp	Ala	Val	Val	Pro	Ala	Leu	Trp	Asp	Val	Ser	His	Ile	Trp	Thr
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His	Pro	Arg	Gln	Ala	Asp	Ser	His	Phe	Asn	Met	Leu	Leu	Pro	Asp	Gly	
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Asn	Glu	Asn	Ala	His	Gln	Leu	Ser	Val	Ala	Leu	Asn	Gln	Val	Ala	His	
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gaa	tcc	gag	tgg	ttt	ggc	acc	ctg	acc	gac	atc	gag	cag	gat	tta	ttg	547
Glu	Ser	Glu	Trp	Phe	Gly	Thr	Leu	Thr	Asp	Ile	Glu	Gln	Asp	Leu	Leu	
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 35 40 45
 Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
 50 55 60
 Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
 65 70 75 80
 Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
 85 90 95
 Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
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 115 120 125
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 Val Thr Ile Ser Arg
 1 5
 cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa 163
 Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
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 act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc 211

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Leu	Leu	Ala	Leu	Asp	Phe	Gln	Leu	Thr	Val	Glu	Glu	Tyr	Glu	Thr	Ile	
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Phe	Ser	Leu	Ala	Asp	Leu	Asn	Arg	Arg	Glu	Tyr	Val	Gly	Leu	Ile	Gln	
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Ile	Asp	His	Thr	Arg	Ala	Glu	Asn	Gln	Gly	Trp	Asp	Ser	Gly	Glu	Asp	
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Phe	Ala	Ser	Tyr	Ala	Lys	Ser	Val	Phe	Ser	Ser	Gly	Asp	Asn	Leu	Leu	
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Thr	Thr	Glu	Ser	Leu	Lys	Gln	Leu	Val	Thr	His	Ile	Pro	Ala	Arg	Ser	
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Leu	Lys	Asp	Leu	Asn	Glu	Val	Glu	Ala	Phe	Val	Gly	Thr	His	Gly	Leu	
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ccg	gaa	ttg	tct	ttc	aaa	ttt	ctt	ctg	gag	tgt	ctg	agc	ggc	gaa	gct	931
Pro	Glu	Leu	Ser	Phe	Lys	Phe	Leu	Leu	Glu	Cys	Leu	Ser	Gly	Glu	Ala	

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cca Pro	gaa Glu	tggt Trp	aca Thr	gtg Val 330	att Ile	tat Tyr	gac Asp	gga Gly	aac Asn 335	tcc Ser	att Ile	aaa Lys	gtt Val	cgt Arg 340	ccc Pro	1123			
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gac Asp	aaa Lys 360	ccg Pro	ctc Leu	tcc Ser	agc Ser	ttg Leu	aga Arg 365	gtc Val	atc Ile	act Thr	cca Pro	aca Thr 370	gag Glu	aaa Lys	tcc Ser	1219			
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Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu Ser Asp Asp Pro Trp	
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Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser Thr Lys Thr Thr Leu	
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Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys Met Val Ala Tyr Lys	
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Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser Lys Ile Gly Ser Ser	
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Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys Arg Thr Gly Lys Ile	
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950 955 960 965	
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Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser	
970 975 980	
gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc	3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile	
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 <213> Corynebacterium glutamicum

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 Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
 35 40 45
 Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
 50 55 60
 Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
 65 70 75 80
 Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
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 Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
 100 105 110
 Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
 115 120 125
 His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
 130 135 140
 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
 145 150 155 160
 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
 165 170 175
 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
 180 185 190
 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
 195 200 205
 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
 210 215 220
 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
 225 230 235 240
 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
 245 250 255
 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
 260 265 270
 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
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Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
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 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
 305 310 315 320
 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
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 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
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 Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
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 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
 370 375 380
 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
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 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
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 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
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 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
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 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
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 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
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 Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
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 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
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 Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
 580 585 590
 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
 595 600 605
 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile

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Asp	Phe	Pro	Glu	Asp 645	Tyr	Asn	Leu	Asp	Val 650	Phe	Ile	Thr	Pro	Pro	Gln 655
Leu	His	Tyr	Gln 660	Val	Pro	Val	Thr	His 665	Ser	Gln	Thr	Lys	Trp 670	Glu	Ser
Thr	Lys	Thr	Thr 675	Leu	Asp	Phe	Asn 680	Asp	Phe	Ala	Asp	Gly 685	Asn	Leu	Gln
Ile 690	Arg	Phe	Pro	Asn	Glu	Val 695	Tyr	Asp	Pro	Asn	Leu 700	Lys	Ile	Ile	Lys
Met 705	Val	Ala	Tyr	Lys	Lys 710	Pro	Glu	Ser	Ser	Glu 715	Pro	Lys	Tyr	Leu	Ser 720
Lys	Ile	Gly	Ser	Ser 725	Lys	Val	Trp	Ser	Ile 730	Pro	Met	Asp	Arg	Ile	Lys 735
Glu	Leu	Met	Asp 740	Asp	Asp	Ala	Gln 745	Phe	Leu	Leu	Ile	Ala	Glu 750	Trp	Phe
Ala	Glu	Ser 755	Lys	Asp	Gln	His	Arg 760	Glu	Lys	Ile	Ile	Ser 765	Glu	Ala	Lys
Arg	Thr 770	Gly	Lys	Ile	Ser	Asn 775	Ala	Ala	Leu	Lys	Ser 780	Ala	Arg	Pro	Gln
Pro 785	Gln	Ala	Ser	Ser 790	His	Ile	Ala	Thr	Ile	Glu 795	Lys	Lys	Pro	Leu	Leu 800
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His	Thr	Ser	Lys 820	Arg	Leu	Glu	Gly	Trp 825	Ala	Trp	Ser	Ala	Leu	Asn 830	Pro
Leu	Asp	Pro 835	Pro	Ile	Lys	Val	Asp 840	Phe	Gln	Gly	Thr	Ser 845	Gly	Ser	Leu
Pro 850	Asp	Thr	His	Phe	Val	Val 855	Gly	Pro	Leu	Ile	Val 860	Glu	Val	Arg	Glu
Lys 865	Glu	Phe	Leu	Ser	Gln 870	Trp	Gln	Pro	Lys	Val 875	Pro	Ser	Val	Lys	Ala 880
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Phe	Leu	Thr	His 900	Arg	Trp	Met	Phe	Ala 905	Pro	Arg	Ser	Gly	Lys 910	Val	Leu
Leu	Pro	Gln	Glu 915	Ile	Arg	Thr	Val 920	Trp	Asp	Ala	Arg	Phe	Asn	Met	Arg
His 930	Val	Leu	Ala	Gln	Arg	Glu 935	Asn	Leu	His	Val	Lys 940	Ser	Ile	Gln	Asp

Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
 945 950 955 960
 Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
 965 970 975
 Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
 980 985 990
 Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
 995 1000 1005
 Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
 1010 1015 1020
 Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
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 Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
 1045 1050 1055
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 1075 1080 1085
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 Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr
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 Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
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 Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
 1140 1145 1150
 Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
 1155 1160 1165
 Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
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 Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
 1185 1190 1195 1200
 Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(982)

<223> RXN02506

<400> 289

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atatccatct cttgcataacc ggccgaaagg tttagcacac atg cac ctc aat cag 115
                                         Met His Leu Asn Gln
                                         .1 5

ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
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gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc 211
Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
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gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc 259
Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe Glu Arg His Ser Arg
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ggg gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc 307
Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu
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cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt 355
Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly
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gag cac ctc atc acc agc atc aac atc gga gtt ccc cct gga atc ccc 403
Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro
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atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc 451
Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg
                        105 110 115

att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa 499
Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys
                        120 125 130

caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt 547
Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe
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gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa 595
Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys
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aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc 643
Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu
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ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta 691
Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val

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Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val			
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aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc			787
Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile			
215	220	225	
gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc			835
Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala			
230	235	240	245
cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac			883
Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp			
250	255	260	
gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc			931
Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro			
265	270	275	
caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga			979
Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln Lys Phe Ile Asp Gly			
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Asn			

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<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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		20						25					30		

Ser	Arg	Gln	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Val	Gly	Ala	Pro	Leu	Phe
		35					40					45			

Glu	Arg	His	Ser	Arg	Gly	Val	Ser	Leu	Thr	Lys	Ala	Gly	Glu	Ile	Leu
	50					55					60				

His	Glu	Glu	Ala	Leu	Arg	Thr	Leu	Ser	Arg	Met	Gln	Ser	Val	Val	Asp
	65				70					75					80

Glu	Ile	Gln	Ser	Gly	Glu	His	Leu	Ile	Thr	Ser	Ile	Asn	Ile	Gly	Val
				85					90					95	

Pro	Pro	Gly	Ile	Pro	Ile	Asp	Trp	Leu	Arg	Cys	Gln	Leu	Ile	Asp	Leu
			100					105					110		

Gly	Pro	Glu	Thr	Arg	Ile	Ser	Leu	Ile	Glu	Ser	Pro	Thr	Asp	Asp	Gln
		115					120					125			

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
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 Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
 145 150 155 160
 Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
 165 170 175
 Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
 180 185 190
 Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
 195 200 205
 Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
 210 215 220
 Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
 225 230 235 240
 Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
 245 250 255
 Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
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 Lys Phe Ile Asp Gly Asn
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 <222> (101)..(766)
 <223> RXN02620

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 Met Ala Gly Ala Val
 1 5
 gga cgc ccc cgg aga tca gct ccg cga cgg gca ggc aag aat cct cgc 163
 Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg
 10 15 20
 gag gag att ctt gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc 211
 Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe
 25 30 35
 gca aca acc tcc acg cat caa atc gct gat gcc gtg gga atc cgc caa 259
 Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln

40	45	50	
gcc tcg ctg tat tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc			307
Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr			
55	60	65	
ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta			355
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu			
70	75	80	85
agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc			403
Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala			
	90	95	100
tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg			451
Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu			
	105	110	115
tac caa ctc ccc atc gtt ggt tct gaa gag ttc gcc gag tac cac agc			499
Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser			
	120	125	130
cag cgc gaa gcc ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc			547
Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile			
	135	140	145
gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg			595
Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser			
150	155	160	165
gtg atc gaa atg cgt cgc aac gac ggc aag att cca agc ccg ctt tcc			643
Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser			
	170	175	180
gca gac agc ctc ccg gag acc gca att atg ctt gcc gac gcc tcc ctc			691
Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu			
	185	190	195
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Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu			
	200	205	210
gaa cta atc aag cag gct gac gcg aaa taaccatccg cgctgcgaa atc			789
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<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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			20					25					30		

Thr	Arg	Gln	Gly	Phe	Ala	Thr	Thr	Ser	Thr	His	Gln	Ile	Ala	Asp	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45					
Val	Gly	Ile	Arg	Gln	Ala	Ser	Leu	Tyr	Tyr	His	Phe	Pro	Ser	Lys	Thr
50						55					60				
Glu	Ile	Phe	Leu	Thr	Leu	Leu	Lys	Ser	Thr	Val	Glu	Pro	Ser	Thr	Val
65					70					75					80
Leu	Ala	Glu	Asp	Leu	Ser	Thr	Leu	Asp	Ala	Gly	Pro	Glu	Met	Arg	Leu
				85					90					95	
Trp	Ala	Ile	Val	Ala	Ser	Glu	Val	Arg	Leu	Leu	Leu	Ser	Thr	Lys	Trp
			100					105						110	
Asn	Val	Gly	Arg	Leu	Tyr	Gln	Leu	Pro	Ile	Val	Gly	Ser	Glu	Glu	Phe
		115					120					125			
Ala	Glu	Tyr	His	Ser	Gln	Arg	Glu	Ala	Leu	Thr	Asn	Val	Phe	Arg	Asp
	130					135					140				
Leu	Ala	Thr	Glu	Ile	Val	Gly	Asp	Asp	Pro	Arg	Ala	Glu	Leu	Pro	Phe
145					150					155					160
His	Ile	Thr	Met	Ser	Val	Ile	Glu	Met	Arg	Arg	Asn	Asp	Gly	Lys	Ile
				165					170					175	
Pro	Ser	Pro	Leu	Ser	Ala	Asp	Ser	Leu	Pro	Glu	Thr	Ala	Ile	Met	Leu
			180					185						190	
Ala	Asp	Ala	Ser	Leu	Ala	Val	Leu	Gly	Ala	Pro	Leu	Pro	Ala	Asp	Arg
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Val	Glu	Lys	Thr	Leu	Glu	Leu	Ile	Lys	Gln	Ala	Asp	Ala	Lys		
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<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(631)

<223> RXN00826

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				Met	Ile	Thr	Val	Leu	
				1				5	

att	gat	gga	caa	tcc	ggt	gcg	ggc	aaa	acc	acc	ttg	gcg	ggt	gag	tta	163
Ile	Asp	Gly	Gln	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ala	Gly	Glu	Leu	
				10				15						20		

gct	gcc	cgc	acc	ggg	ttt	cag	ttg	ggt	cat	ttg	gat	gac	ttt	tat	cct	211
Ala	Ala	Arg	Thr	Gly	Phe	Gln	Leu	Val	His	Leu	Asp	Asp	Phe	Tyr	Pro	
			25				30						35			

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 Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
 55 60 65
 tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
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 70 75 80 85
 gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tgc ctg 403
 Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
 90 95 100
 ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
 Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
 105 110 115
 aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
 Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
 120 125 130
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 Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
 135 140 145
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 Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
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 gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641
 Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
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<211> 177

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<400> 294

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 35 40 45
 Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
 50 55 60
 Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
 65 70 75 80
 Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys

85										90					95															
Arg	Lys	Ala	Ser	Leu	Leu	Gly	Glu	Leu	Val	Thr	Val	Arg	Ile	Thr	Gly															
			100					105					110																	
Pro	Glu	Ala	Leu	Arg	Lys	Gln	Arg	Ala	Leu	Asn	Arg	Asp	Pro	Asp	Tyr															
		115					120					125																		
Ala	Pro	Phe	Trp	Lys	Val	Trp	Ala	Gln	Gln	Glu	Gln	Arg	His	Phe	Ser															
	130					135						140																		
Leu	Gly	Val	Glu	Val	Asp	His	Glu	Ile	Val	Leu	Gly	Ser	Asp	Glu	Ala															
145					150					155				160																
Ser	Gly	Arg	Pro	Glu	Glu	Ile	Tyr	Asp	Ser	Leu	Gly	Thr	Ala	Gln	Ser															
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Ser

<210> 295
 <211> 555
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(532)
 <223> RXS00070

<400> 295
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 actatcgaag tacattttgt gtcattgagg aggatcaacg gtg ggt atc aat cgc 115
 Val Gly Ile Asn Arg 5
 1
 atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163
 Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln 20
 10 15
 cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211
 Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser 35
 25 30
 gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259
 Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly 50
 40 45
 ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307
 Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala 65
 55 60
 gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355
 Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys 85
 70 75 80
 cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403
 His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg 100
 90 95

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451
 Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
 105 110 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499
 Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
 120 125 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
 Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 135 140

ctg 555

<210> 296

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
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Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
 20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
 35 40 45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
 50 55 60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
 65 70 75 80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
 85 90 95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
 100 105 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
 115 120 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 130 135 140

<210> 297

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXS00133

<400> 297

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aatttgaagg tggataccca gcggattaaa gatgatgaag atg cta ttc gtt cgg 115
 Met Leu Phe Val Arg
 1 5

cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc 163
 Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
 10 15 20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211
 Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
 25 30 35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259
 Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly
 40 45 50

gtt ggt gga cgc gtc gtc gca acc cgt cgt ccg gtt ggt gtg agt gat 307
 Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro Val Gly Val Ser Asp
 55 60 65

tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag 355
 Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln
 70 75 80 85

gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc 403
 Asp Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg
 90 95 100

gaa att cgt ggc gtt ttg tat gtt ggc gtt cac tct gcg gtg cgt ctc 451
 Glu Ile Arg Gly Val Leu Tyr Val Gly Val His Ser Ala Val Arg Leu
 105 110 115

ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa 499
 Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu
 120 125 130

caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat 547
 Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp
 135 140 145

ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg 595
 Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp
 150 155 160 165

gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt 643
 Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg
 170 175 180

gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag 691
 Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln
 185 190 195

atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt 739
 Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg
 200 205 210

gag ttg gac gtg ctg gct tgt gtc gcg ctc ggt cac acc aac gtc gaa 787
 Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly His Thr Asn Val Glu
 215 220 225

gct gct gaa gag atg ggc atc ggc gcg gaa acc gtc aag agc tac ctg 835
 Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr Val Lys Ser Tyr Leu
 230 235 240 245

cgc tcg gtc atg cgc aag ctc ggc gcc cac acg cgc tac gag gca gtc 883
 Arg Ser Val Met Arg Lys Leu Gly Ala His Thr Arg Tyr Glu Ala Val
 250 255 260

aac gca gca cgc cgg atc ggc gca ctg cct taaaaagatt ttgctttacg acg 936
 Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
 265 270

<210> 298

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Leu Phe Val Arg Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile
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Pro Val Thr Met Phe Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile
 20 25 30

Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile
 35 40 45

Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro
 50 55 60

Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys
 65 70 75 80

Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro
 85 90 95

Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His
 100 105 110

Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr
 115 120 125

Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg
 130 135 140

Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met
 145 150 155 160

Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg
 165 170 175

Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu
 180 185 190

Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr

195	200	205
Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly		
210	215	220
His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr		
225	230	235
Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr		
245	250	255
Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro		
260	265	270

<210> 299

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXS00144

<400> 299

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ctttaacgga ccgcacagag aggcggggaa ggaggtcacg atg agc gaa cgt aat	115
Met Ser Glu Arg Asn	
1 5	

agt gct gta cta gaa ctc ctt aat gag gac gac gtc agc cgt acc atc	163
Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp Val Ser Arg Thr Ile	
10 15 20	

gca cgc atc gcg cac cag att att gag aaa acc gcg ctt gat tcc aaa	211
Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr Ala Leu Asp Ser Lys	
25 30 35	

gac gcg gat cgg gtc atg ttg tta ggt att ccc tca ggt gga gtc cca	259
Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro Ser Gly Gly Val Pro	
40 45 50	

ttg gcc cgt agg ctc gct gaa aag atc gaa gaa ttt tcc ggc gtt tcg	307
Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu Phe Ser Gly Val Ser	
55 60 65	

gta gat acc ggc gct gtt gat atc acc ttg tac agg gat gat ctt cga	355
Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr Arg Asp Asp Leu Arg	
70 75 80 85	

aac aaa cca cac cgc gca ctg cag ccc acc tct att cca gca ggt ggt	403
Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser Ile Pro Ala Gly Gly	
90 95 100	

atc gat aac acc acc gtg att ttg gtg gat gat gtg ctg ttt tcc ggt	451
Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp Val Leu Phe Ser Gly	
105 110 115	

cgt acc atc cgc gct gca ctt gat gct ttg cgc gac gtt gga cgc ccc	499
---	-----

Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg Asp Val Gly Arg Pro
 120 125 130
 aac tac atc cag tta gct gtg ttg gtt gac cgc ggt cat cgc cag ctg 547
 Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg Gly His Arg Gln Leu
 135 140 145
 ccc att cgc gct gac tat gtg ggc aaa aat ctc ccc acc gca cgc gcg 595
 Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu Pro Thr Ala Arg Ala
 150 155 160 165
 gaa gac gtt tcc gtc atg ctt aca gaa atc gac ggc cgc gat gca gtc 643
 Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp Gly Arg Asp Ala Val
 170 175 180
 acg ctc acc cga gaa gac tct gaa ggg gat tcc tagatgaagc acctcctatc 696
 Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser
 185 190
 cat 699

<210> 300
 <211> 192
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 300
 Met Ser Glu Arg Asn Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp
 1 5 10 15
 Val Ser Arg Thr Ile Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr
 20 25 30
 Ala Leu Asp Ser Lys Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro
 35 40 45
 Ser Gly Gly Val Pro Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu
 50 55 60
 Phe Ser Gly Val Ser Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr
 65 70 75 80
 Arg Asp Asp Leu Arg Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser
 85 90 95
 Ile Pro Ala Gly Gly Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp
 100 105 110
 Val Leu Phe Ser Gly Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg
 115 120 125
 Asp Val Gly Arg Pro Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg
 130 135 140
 Gly His Arg Gln Leu Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu
 145 150 155 160
 Pro Thr Ala Arg Ala Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp
 165 170 175

Gly Arg Asp Ala Val Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser
 180 185 190

<210> 301
 <211> 1230
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1207)
 <223> RXS00205

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 atcccacaat aggggtacct tccagaaagt tgggtgaggag atg gct tcc gaa acc 115
 Met Ala Ser Glu Thr
 1 5
 tcc agc ccg aag aag cgg gcc acc acg ctc aaa gac atc gcg caa gca 163
 Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys Asp Ile Ala Gln Ala
 10 15 20
 aca cag ctt tca gtc agc acg gtg tcc cgg gca ttg gcc aac aac gcg 211
 Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala Leu Ala Asn Asn Ala
 25 30 35
 agc att ccg gaa tcc aca cgc atc cga gtg gtt gaa gcc gct caa aag 259
 Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val Glu Ala Ala Gln Lys
 40 45 50
 ctg aac tac cgt ccc aat gcc caa gct cgt gca ttg cgg aag tcg agg 307
 Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala Leu Arg Lys Ser Arg
 55 60 65
 aca gac acc atc ggt gtc atc att cca aac att gag aac cca tat ttc 355
 Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile Glu Asn Pro Tyr Phe
 70 75 80 85
 tcc tca cta gca gca tcg att caa aaa gct gct cgt gaa gct ggg gtg 403
 Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala Arg Glu Ala Gly Val
 90 95 100
 tcc acc att ttg tcc aac tct gaa gaa aac cca gag ctg ctt ggt cag 451
 Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro Glu Leu Leu Gly Gln
 105 110 115
 act ttg gcg atc atg gat gac caa cgc ctc gat gga atc atc gtg gtg 499
 Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp Gly Ile Ile Val Val
 120 125 130
 cca cac att cag tca gag gaa caa gtc act gac ttg gtt aac agg gga 547
 Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp Leu Val Asn Arg Gly
 135 140 145
 gtg cca gta gtg ctg gca gac cgt agt ttt gtt aac tcg tct att cct 595

Val 150	Pro	Val	Val	Leu	Ala 155	Asp	Arg	Ser	Phe	Val 160	Asn	Ser	Ser	Ile	Pro 165	
tcg	gtt	acc	tca	gat	cca	gtt	ccg	ggc	atg	act	gaa	gct	gtg	gac	tta	643
Ser	Val	Thr	Ser	Asp 170	Pro	Val	Pro	Gly	Met 175	Thr	Glu	Ala	Val	Asp 180	Leu	
ctc	ctg	gca	gct	gac	gtg	caa	ttg	ggc	tac	ctt	gcc	ggc	ccg	cag	gat	691
Leu	Leu	Ala	Ala	Asp 185	Val	Gln	Leu	Gly	Tyr 190	Leu	Ala	Gly	Pro	Gln	Asp	
act	tcc	act	ggt	cag	ctg	cgt	ctt	aac	act	ttt	gaa	aga	cta	tgc	gtg	739
Thr	Ser	Thr	Gly	Gln	Leu	Arg	Leu	Asn	Thr	Phe	Glu	Arg	Leu	Cys	Val	
		200					205					210				
gac	cgc	ggc	atc	gtc	gga	gca	tct	gtc	tat	tac	ggt	ggc	tac	cgc	caa	787
Asp	Arg	Gly	Ile	Val	Gly	Ala	Ser	Val	Tyr	Tyr	Gly	Gly	Tyr	Arg	Gln	
	215					220					225					
gaa	tct	gga	tat	gac	ggc	atc	aag	gtg	ctg	atc	aag	cag	gga	gcc	aat	835
Glu	Ser	Gly	Tyr	Asp	Gly	Ile	Lys	Val	Leu	Ile	Lys	Gln	Gly	Ala	Asn	
230					235					240					245	
gcg	att	atc	gct	ggt	gac	tcc	atg	atg	acc	atc	ggt	gcg	ttg	ttg	gct	883
Ala	Ile	Ile	Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Ala	Leu	Leu	Ala	
				250					255						260	
ctt	cat	gag	atg	aat	ttg	aag	atc	ggt	gag	gat	gtg	cag	ctc	att	ggg	931
Leu	His	Glu	Met	Asn	Leu	Lys	Ile	Gly	Glu	Asp	Val	Gln	Leu	Ile	Gly	
			265					270					275			
ttt	gat	aac	aac	cca	att	ttc	cgg	ctg	cag	aat	cca	ccg	ctg	agc	atc	979
Phe	Asp	Asn	Asn	Pro	Ile	Phe	Arg	Leu	Gln	Asn	Pro	Pro	Leu	Ser	Ile	
		280					285					290				
att	gac	cag	cac	gta	caa	gag	atc	ggt	aag	cgt	gcg	ttt	gag	att	ctg	1027
Ile	Asp	Gln	His	Val	Gln	Glu	Ile	Gly	Lys	Arg	Ala	Phe	Glu	Ile	Leu	
	295					300					305					
cag	aag	ctg	atc	aat	ggg	gac	acc	gcg	caa	aaa	tct	gtg	gtg	att	cca	1075
Gln	Lys	Leu	Ile	Asn	Gly	Asp	Thr	Ala	Gln	Lys	Ser	Val	Val	Ile	Pro	
310					315					320					325	
acg	cag	ctc	agc	atc	aat	gga	tca	acg	gcg	gtt	tcc	caa	aag	gcg	gcc	1123
Thr	Gln	Leu	Ser	Ile	Asn	Gly	Ser	Thr	Ala	Val	Ser	Gln	Lys	Ala	Ala	
				330					335					340		
gca	aag	gca	gca	aaa	gca	gcc	caa	aaa	gca	gcc	gcg	aaa	gcc	gca	cag	1171
Ala	Lys	Ala	Ala	Lys	Ala	Ala	Gln	Lys	Ala	Ala	Ala	Lys	Ala	Ala	Gln	
			345					350					355			
aac	acg	caa	cac	gag	gtg	agc	cta	gat	ggt	gaa	ctc	tga	aca	agcg		1217
Asn	Thr	Gln	His	Glu	Val	Ser	Leu	Asp	Gly	Glu	Leu					
		360					365									
ctt	cat	cag	atg													1230

<210> 302

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Ala Ser Glu Thr Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys
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 Leu Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val
 35 40 45
 Glu Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala
 50 55 60
 Leu Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile
 65 70 75 80
 Glu Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala
 85 90 95
 Arg Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro
 100 105 110
 Glu Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp
 115 120 125
 Gly Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp
 130 135 140
 Leu Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg Ser Phe Val
 145 150 155 160
 Asn Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr
 165 170 175
 Glu Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu
 180 185 190
 Ala Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe
 195 200 205
 Glu Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr
 210 215 220
 Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile
 225 230 235 240
 Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile
 245 250 255
 Gly Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp
 260 265 270
 Val Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn
 275 280 285
 Pro Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg
 290 295 300
 Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys

305		310		315		320
Ser Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val						
		325		330		335
Ser Gln Lys Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala						
		340		345		350
Ala Lys Ala Ala Gln Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu						
		355		360		365

Leu

<210> 303
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXS00470

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 ctcatagact ctattgtgga gtgttgaggc tgataagtga atg ggg gaa agc cct 115
 Met Gly Glu Ser Pro
 1 5
 gaa aag gtg gcg ttc agg gtc ttc cct gat ggt ttg gtg tcg cag ggg 163
 Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly Leu Val Ser Gln Gly
 10 15 20
 cat gac atg atc gaa gat atg agt aac aca cct gcg cct tat acc ccg 211
 His Asp Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro
 25 30 35
 cag cct gcg ggg caa gcg gtg cct tta tat ccc acg ttt acc cgg tca 259
 Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro Thr Phe Thr Arg Ser
 40 45 50
 aga gat ggt cgg gtt gtt gcg ggt gtc gca tcg ggg ctg gca aag cat 307
 Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser Gly Leu Ala Lys His
 55 60 65
 ctt aat gtg tcg gtg ttt tgg gtt cgt gcg ctg ctg att ttt gcg gcg 355
 Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu Leu Ile Phe Ala Ala
 70 75 80 85
 ttg ctg agc ggt gcg ggt ctt ttt gcg tat gcc ttg att tgg att ttt 403
 Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala Leu Ile Trp Ile Phe
 90 95 100
 acg cgc att gag aaa aag ggg agt ggg gag gcg tcg aca agc aag cgc 451
 Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala Ser Thr Ser Lys Arg
 105 110 115
 tgg gtg tcg tgg tgc ctg gtg ctg ctc gct atc ggt ggt gct gcg gcg 499

Trp	Val	Ser	Trp	Cys	Leu	Val	Leu	Leu	Ala	Ile	Gly	Gly	Ala	Ala	Ala		
		120					125					130					
tcg	gtg	atg	ctg	agc	acc	ggc	ttc	gcg	gtg	ggc	acg	ttg	gtg	ccc	atc	547	
Ser	Val	Met	Leu	Ser	Thr	Gly	Phe	Ala	Val	Gly	Thr	Leu	Val	Pro	Ile		
	135					140					145						
ggc	gtg	gtc	ggc	gtg	ggc	ctg	ttg	atg	gtg	tgg	ctg	gcg	tat	gac	cgc	595	
Gly	Val	Val	Gly	Val	Gly	Leu	Leu	Met	Val	Trp	Leu	Ala	Tyr	Asp	Arg		
150					155					160					165		
ggg	gtg	gaa	tcc	ggc	ccg	aat	ctg	ctg	att	att	gcc	acc	ggc	ggc	gtg	643	
Gly	Val	Glu	Ser	Gly	Pro	Asn	Leu	Leu	Ile	Ile	Ala	Thr	Gly	Gly	Val		
				170					175					180			
ttg	atg	ctg	gtg	gcg	atc	gtg	ctg	atc	gtg	atg	aat	tgg	aac	acc	cag	691	
Leu	Met	Leu	Val	Ala	Ile	Val	Leu	Ile	Val	Met	Asn	Trp	Asn	Thr	Gln		
			185					190					195				
gac	ggc	ttc	gtc	atg	gcg	ctg	gtg	gcc	gtg	gtg	ctc	acg	ctg	gtg	ggc	739	
Asp	Gly	Phe	Val	Met	Ala	Leu	Val	Ala	Val	Val	Leu	Thr	Leu	Val	Gly		
		200					205					210					
gtg	gct	gcg	ctg	ggc	gtt	ccg	ctg	tgg	gtg	cgg	atg	tgg	gat	cag	ctg	787	
Val	Ala	Ala	Leu	Gly	Val	Pro	Leu	Trp	Val	Arg	Met	Trp	Asp	Gln	Leu		
	215					220					225						
ggc	gag	gag	cgc	gcg	gaa	aaa	gcc	gca	gct	gct	gag	cgc	gca	gat	att	835	
Gly	Glu	Glu	Arg	Ala	Glu	Lys	Ala	Ala	Ala	Ala	Glu	Arg	Ala	Asp	Ile		
230					235					240					245		
gct	tcc	cgc	ctg	cat	gat	tcg	gta	ctg	cag	acc	ttg	gcg	ctg	att	caa	883	
Ala	Ser	Arg	Leu	His	Asp	Ser	Val	Leu	Gln	Thr	Leu	Ala	Leu	Ile	Gln		
				250					255					260			
aag	cgt	gcc	gac	gac	ccc	gcc	gaa	gtc	gcc	cgc	ctg	gcc	cgc	ggg	cag	931	
Lys	Arg	Ala	Asp	Asp	Pro	Ala	Glu	Val	Ala	Arg	Leu	Ala	Arg	Gly	Gln		
			265					270					275				
gaa	cgc	gag	ctg	cgt	caa	tgg	ctg	ttt	gat	tcc	caa	gat	aaa	aca	cct	979	
Glu	Arg	Glu	Leu	Arg	Gln	Trp	Leu	Phe	Asp	Ser	Gln	Asp	Lys	Thr	Pro		
		280					285					290					
caa	aca	acc	ggc	act	gtc	ttt	act	gcg	ttg	gag	cgc	gcc	tgc	ggc	gaa	1027	
Gln	Thr	Thr	Gly	Thr	Val	Phe	Thr	Ala	Leu	Glu	Arg	Ala	Cys	Gly	Glu		
	295					300					305						
gtc	gag	gat	att	tac	gct	ctg	cgt	atc	gtg	cct	gtg	acc	gtg	gga	acc	1075	
Val	Glu	Asp	Ile	Tyr	Ala	Leu	Arg	Ile	Val	Pro	Val	Thr	Val	Gly	Thr		
310					315					320					325		
gat	gaa	gcg	ctg	act	gag	aaa	acg	cag	gca	gcg	gtg	atg	gca	gtc	cgc	1123	
Asp	Glu	Ala	Leu	Thr	Glu	Lys	Thr	Gln	Ala	Ala	Val	Met	Ala	Val	Arg		
				330					335					340			
gaa	gca	ctc	gtg	aac	gtg	gcc	aag	cat	gcc	ggc	gtg	gaa	acc	gcc	gat	1171	
Glu	Ala	Leu	Val	Asn	Val	Ala	Lys	His	Ala	Gly	Val	Glu	Thr	Ala	Asp		
			345					350					355				
gtg	tac	gcc	gaa	att	atg	ctc	ggc	gaa	ctg	aac	att	ttc	gtc	cgc	gac	1219	
Val	Tyr	Ala	Glu	Ile	Met	Leu	Gly	Glu	Leu	Asn	Ile	Phe	Val	Arg	Asp		

360	365	370	
cgc ggt gca gga ttc gac ccc gac aac atc ccc gac ggg cac cac ggg			1267
Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly			
375	380	385	
ctc gcc gaa tcc gtc caa ggc cgc gtc gaa cga gcc ggc gga aaa gta			1315
Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val			
390	395	400	405
cgc atc aaa tct gaa atc ggc gaa ggc acc gaa gtg gca atc acc atg			1363
Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met			
410	415	420	
gat gtg tagttggtcg tacgcgcgtg tct			1392
Asp Val			

<210> 304

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Gly Glu Ser Pro Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly	
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Leu Val Ser Gln Gly His Asp Met Ile Glu Asp Met Ser Asn Thr Pro	
20 25 30	

Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro	
35 40 45	

Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser	
50 55 60	

Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu	
65 70 75 80	

Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala	
85 90 95	

Leu Ile Trp Ile Phe Thr Arg Ile Glu Lys Lys Gly Ser Gly Glu Ala	
100 105 110	

Ser Thr Ser Lys Arg Trp Val Ser Trp Cys Leu Val Leu Leu Ala Ile	
115 120 125	

Gly Gly Ala Ala Ala Ser Val Met Leu Ser Thr Gly Phe Ala Val Gly	
130 135 140	

Thr Leu Val Pro Ile Gly Val Val Gly Val Gly Leu Leu Met Val Trp	
145 150 155 160	

Leu Ala Tyr Asp Arg Gly Val Glu Ser Gly Pro Asn Leu Leu Ile Ile	
165 170 175	

Ala Thr Gly Gly Val Leu Met Leu Val Ala Ile Val Leu Ile Val Met	
180 185 190	

Asn Trp Asn Thr Gln Asp Gly Phe Val Met Ala Leu Val Ala Val Val
 195 200 205
 Leu Thr Leu Val Gly Val Ala Ala Leu Gly Val Pro Leu Trp Val Arg
 210 215 220
 Met Trp Asp Gln Leu Gly Glu Glu Arg Ala Glu Lys Ala Ala Ala Ala
 225 230 235 240
 Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr
 245 250 255
 Leu Ala Leu Ile Gln Lys Arg Ala Asp Asp Pro Ala Glu Val Ala Arg
 260 265 270
 Leu Ala Arg Gly Gln Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser
 275 280 285
 Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu
 290 295 300
 Arg Ala Cys Gly Glu Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro
 305 310 315 320
 Val Thr Val Gly Thr Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Ala
 325 330 335
 Val Met Ala Val Arg Glu Ala Leu Val Asn Val Ala Lys His Ala Gly
 340 345 350
 Val Glu Thr Ala Asp Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn
 355 360 365
 Ile Phe Val Arg Asp Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro
 370 375 380
 Asp Gly His His Gly Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg
 385 390 395 400
 Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu
 405 410 415
 Val Ala Ile Thr Met Asp Val
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<210> 305

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXS00471

<400> 305

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 ggctgtacgc gcgtgtcttc ggggctgtaa cctgaaaggc atg gtt gat gtg ttt 115
 Met Val Asp Val Phe

	1	5	
ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta			163
Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu			
	10	15	20
ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc			211
Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala			
	25	30	35
gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc			259
Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val			
	40	45	50
cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac			307
His Met Pro Asp Gly Gly Gly Leu Ala Val Leu Gln Gln Ile Asn Asp			
	55	60	65
tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg			355
Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala			
	70	75	85
gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc			403
Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr			
	90	95	100
aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa			451
Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys			
	105	110	115
tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac			499
Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp			
	120	125	130
gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca			547
Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala			
	135	140	145
ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca			595
Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro			
	150	155	160
gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta			643
Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu			
	170	175	180
gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc			691
Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser			
	185	190	195
gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa			739
Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln			
	200	205	210
caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt			787
Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu			
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gac taatggcggc taaaaagagt ggc			813
Asp			
230			

<210> 306

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Met Val Asp Val Phe Leu Val Asp Asp His Ser Val Phe Arg Ser Gly
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Thr Val Ala Asp Ala Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val
 35 40 45

Val Leu Leu Asp Val His Met Pro Asp Gly Gly Gly Leu Ala Val Leu
 50 55 60

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser
 65 70 75 80

Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala
 85 90 95

Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala
 100 105 110

Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala
 115 120 125

Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala
 130 135 140

Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys
 145 150 155 160

Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu
 165 170 175

Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys
 180 185 190

Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile
 195 200 205

Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala
 210 215 220

His Ser Arg Asp Leu Asp
 225 230

<210> 307

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXS00481

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aaataaaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag 115
                                         Met Leu Asn Met Gln
                                         1 5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat 163
Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
                        10 15 20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc 211
Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
                        25 30 35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg 259
Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
                        40 45 50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt 307
Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
                        55 60 65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att 355
Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
                        70 75 80 85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct 403
Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
                        90 95 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta 451
His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
                        105 110 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg 499
Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
                        120 125 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg 547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
                        135 140 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta 595
Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
                        150 155 160 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca 643
Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
                        170 175 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag 685
Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
                        185 190 195

tagatgacca tctacgttaa tta 708

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<223> RXS00649
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cattttgtgc aagatgcaat agctggcaaa ctggagagacc atg agc acc gac ccc 115
Met Ser Thr Asp Pro
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1 5
 atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163
 Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
 10 15 20
 caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211
 Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
 25 30 35
 ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259
 Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
 40 45 50
 ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307
 Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
 55 60 65
 cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355
 Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
 70 75 80 85
 ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403
 Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
 90 95 100
 gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451
 Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
 105 110 115
 tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499
 Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
 120 125 130
 ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547
 Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
 135 140 145
 ccg cgc ccc tgactcagcc caagccagag ccc 579
 Pro Arg Pro
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<210> 310

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe
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 Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
 20 25 30
 Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
 35 40 45
 Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
 50 55 60

Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
 65 70 75 80
 Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
 85 90 95
 Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
 100 105 110
 Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
 115 120 125
 Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
 130 135 140
 Val Gly Lys His Trp Pro Arg Pro
 145 150

<210> 311
 <211> 759
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(736)
 <223> RXS00650

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 Met Ile Arg Val Leu
 1 5
 ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg 163
 Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu
 10 15 20
 gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa 211
 Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu
 25 30 35
 ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg 259
 Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met
 40 45 50
 gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc 307
 Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly
 55 60 65
 gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa 355
 Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys
 70 75 80 85
 gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca 403
 Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala
 90 95 100
 atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc 451

Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser
 105 110 115
 gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg 499
 Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu
 120 125 130
 tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa 547
 Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys
 135 140 145
 acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt 595
 Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly
 150 155 160 165
 gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc 643
 Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala
 170 175 180
 acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg 691
 Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg
 185 190 195
 tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg 736
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 tagcgggggt tgctgcaagg ctt 759

<210> 312

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

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 20 25 30
 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
 35 40 45
 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
 50 55 60
 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
 65 70 75 80
 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
 85 90 95
 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
 100 105 110
 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
 115 120 125
 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg

130	135	140
Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu		
145	150	155 160
Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu		
	165	170 175
Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp		
	180	185 190
Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu		
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Gln Gly Leu Leu		
210		

<210> 313
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1003)
 <223> RXS00657

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 Met Ser Thr Glu Asp
 1 5
 att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
 10 15 20
 cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211
 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
 25 30 35
 gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
 40 45 50
 cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307
 Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
 55 60 65
 att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag 355
 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
 70 75 80 85
 atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403
 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
 90 95 100
 atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451
 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly

105					110					115						
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Gly	Leu	Ser	Gly	Met	Val	Met	Gly	Ser	Val	Ser	Gly	Ala	Val	Val	Ser	
		120					125					130				
cac	gca	aag	tgt	cca	gtc	gtt	gtt	gtc	cgt	gaa	gac	agc	gca	gtc	aac	547
His	Ala	Lys	Cys	Pro	Val	Val	Val	Val	Arg	Glu	Asp	Ser	Ala	Val	Asn	
		135				140					145					
gaa	gac	agc	aag	tac	ggc	cca	gtc	gtc	gtc	ggt	gtg	gat	ggc	tcc	gaa	595
Glu	Asp	Ser	Lys	Tyr	Gly	Pro	Val	Val	Val	Gly	Val	Asp	Gly	Ser	Glu	
		150			155					160					165	
gtc	tcc	caa	cag	gca	acc	gaa	tac	gca	ttt	gcg	gaa	gct	gaa	gct	cgt	643
Val	Ser	Gln	Gln	Ala	Thr	Glu	Tyr	Ala	Phe	Ala	Glu	Ala	Glu	Ala	Arg	
				170					175						180	
ggc	gcc	gaa	ctc	gtt	gca	gtt	cac	acc	tgg	atg	gac	atg	cag	gta	cag	691
Gly	Ala	Glu	Leu	Val	Ala	Val	His	Thr	Trp	Met	Asp	Met	Gln	Val	Gln	
			185					190					195			
gca	tca	ctt	gca	ggt	ctt	gca	gct	gct	caa	cag	cag	tgg	gat	gaa	gtg	739
Ala	Ser	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Gln	Gln	Gln	Trp	Asp	Glu	Val	
		200				205						210				
gaa	cgt	cag	caa	acc	gac	atg	ctg	atc	gaa	cgc	ctc	gca	cca	ctg	gtg	787
Glu	Arg	Gln	Gln	Thr	Asp	Met	Leu	Ile	Glu	Arg	Leu	Ala	Pro	Leu	Val	
	215					220					225					
gaa	aag	tac	cca	agt	gta	acc	gtc	aag	aag	atc	atc	acc	cgt	gac	cgc	835
Glu	Lys	Tyr	Pro	Ser	Val	Thr	Val	Lys	Lys	Ile	Ile	Thr	Arg	Asp	Arg	
	230				235					240					245	
cca	gtt	cgc	gca	ctt	gca	gaa	gca	tct	gaa	aac	gcg	cag	ctc	cta	gtc	883
Pro	Val	Arg	Ala	Leu	Ala	Glu	Ala	Ser	Glu	Asn	Ala	Gln	Leu	Leu	Val	
				250					255					260		
gtt	ggt	tcc	cat	ggt	cgt	ggc	gga	ttt	aag	ggc	atg	ctc	ctt	ggc	tcc	931
Val	Gly	Ser	His	Gly	Arg	Gly	Gly	Phe	Lys	Gly	Met	Leu	Leu	Gly	Ser	
			265				270						275			
acc	tcc	cgc	gca	ctg	ctg	caa	tcc	gca	ccg	tgc	cca	atg	atg	gtg	gtt	979
Thr	Ser	Arg	Ala	Leu	Leu	Gln	Ser	Ala	Pro	Cys	Pro	Met	Met	Val	Val	
		280				285						290				
cgc	cca	cct	gag	aag	att	aag	aag	tagttttcttt	taagtttcga	tgc						1026
Arg	Pro	Pro	Glu	Lys	Ile	Lys	Lys									
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 <213> Corynebacterium glutamicum

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35					40					45						
Ala	Glu	Gly	Met	Val	Pro	Pro	Gln	Glu	Leu	Phe	Asp	Asp	Leu	Gln	Ala	
50					55					60						
Glu	Ala	Leu	Glu	Lys	Ile	Asn	Glu	Ala	Arg	Asp	Ile	Ala	His	Glu	Val	
65					70					75					80	
Ala	Pro	Glu	Ile	Lys	Ile	Gly	His	Thr	Ile	Ala	Glu	Gly	Ser	Pro	Ile	
85					90					95						
Asp	Met	Leu	Leu	Glu	Met	Ser	Pro	Asp	Ala	Thr	Met	Ile	Val	Met	Gly	
100					105					110						
Ser	Arg	Gly	Leu	Gly	Gly	Leu	Ser	Gly	Met	Val	Met	Gly	Ser	Val	Ser	
115					120					125						
Gly	Ala	Val	Val	Ser	His	Ala	Lys	Cys	Pro	Val	Val	Val	Val	Arg	Glu	
130					135					140						
Asp	Ser	Ala	Val	Asn	Glu	Asp	Ser	Lys	Tyr	Gly	Pro	Val	Val	Val	Gly	
145					150					155					160	
Val	Asp	Gly	Ser	Glu	Val	Ser	Gln	Gln	Ala	Thr	Glu	Tyr	Ala	Phe	Ala	
165					170					175						
Glu	Ala	Glu	Ala	Arg	Gly	Ala	Glu	Leu	Val	Ala	Val	His	Thr	Trp	Met	
180					185					190						
Asp	Met	Gln	Val	Gln	Ala	Ser	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Gln	Gln	
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Gln	Trp	Asp	Glu	Val	Glu	Arg	Gln	Gln	Thr	Asp	Met	Leu	Ile	Glu	Arg	
210					215					220						
Leu	Ala	Pro	Leu	Val	Glu	Lys	Tyr	Pro	Ser	Val	Thr	Val	Lys	Lys	Ile	
225					230					235					240	
Ile	Thr	Arg	Asp	Arg	Pro	Val	Arg	Ala	Leu	Ala	Glu	Ala	Ser	Glu	Asn	
245					250					255						
Ala	Gln	Leu	Leu	Val	Val	Gly	Ser	His	Gly	Arg	Gly	Gly	Phe	Lys	Gly	
260					265					270						
Met	Leu	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Leu	Leu	Gln	Ser	Ala	Pro	Cys	
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Pro	Met	Met	Val	Val	Arg	Pro	Pro	Glu	Lys	Ile	Lys	Lys				
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<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXS00719

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Val Thr Asp Lys His
1 5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163
Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
10 15 20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta 211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
25 30 35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc 259
Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
40 45 50

ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa 307
Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
55 60 65

aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac 355
Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
70 75 80 85

tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa 403
Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
90 95 100

gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa 451
Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
105 110 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa 499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
120 125 130

gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg 547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
135 140 145

ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac 595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
150 155 160 165

gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg 643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Ala Glu Val Ala Met
170 175 180

agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc 691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile
185 190 195

acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg 739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val
200 205 210

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cca gtg atc ttg gtt gcg aac aaa ttc gac tcc gac agc cag tgg gct	787
Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser Asp Ser Gln Trp Ala	
215 220 225	
gac atg gct gag ttc tac agc ctc ggc ctt ggc gat cca tac cca gtt	835
Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly Asp Pro Tyr Pro Val	
230 235 240 245	
tca gcc cag cat gga cgt ggt ggc gct gac gtt ttg gac aaa gtc ctt	883
Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val Leu Asp Lys Val Leu	
250 255 260	
gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct	931
Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro	
265 270 275	
cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg	979
Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu	
280 285 290	
ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca	1027
Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala	
295 300 305	
gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa	1075
Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys	
310 315 320 325	
ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act	1123
Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr	
330 335 340	
gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc	1171
Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile	
345 350 355	
gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc	1219
Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile	
360 365 370	
acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag	1267
Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys	
375 380 385	
gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc	1315
Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg	
390 395 400 405	
cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct	1363
Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro	
410 415 420	
tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag	1411
Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln	
425 430 435	
cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt	1459
Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg	
440 445 450	

atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg 1507
 Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
 455 460 465

 aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc 1555
 Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
 470 475 480 485

 acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc 1603
 Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
 490 495 500

 ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa 1651
 Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
 505 510 515

 cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc 1699
 Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
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 gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttccctaa aag 1752
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 <213> Corynebacterium glutamicum

<400> 316
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 Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
 35 40 45

 Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Phe Asp Ala
 50 55 60

 Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
 65 70 75 80

 Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
 85 90 95

 Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
 100 105 110

 Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
 115 120 125

 Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
 130 135 140

 Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
 145 150 155 160

Gly	Trp	Asp	Pro	Asn	Val	Lys	Gly	Ile	His	Ala	Ser	Ile	Ala	Gln	Gln	
				165					170					175		
Ala	Glu	Val	Ala	Met	Ser	Thr	Ala	Asp	Val	Ile	Val	Phe	Val	Val	Asp	
			180					185					190			
Thr	Lys	Val	Gly	Ile	Thr	Glu	Thr	Asp	Ser	Val	Met	Ala	Ala	Lys	Leu	
		195					200					205				
Leu	Arg	Ser	Glu	Val	Pro	Val	Ile	Leu	Val	Ala	Asn	Lys	Phe	Asp	Ser	
	210					215					220					
Asp	Ser	Gln	Trp	Ala	Asp	Met	Ala	Glu	Phe	Tyr	Ser	Leu	Gly	Leu	Gly	
225					230					235					240	
Asp	Pro	Tyr	Pro	Val	Ser	Ala	Gln	His	Gly	Arg	Gly	Gly	Ala	Asp	Val	
				245					250					255		
Leu	Asp	Lys	Val	Leu	Glu	Leu	Phe	Pro	Glu	Glu	Pro	Arg	Ser	Lys	Ser	
			260					265					270			
Ile	Val	Glu	Gly	Pro	Arg	Arg	Val	Ala	Leu	Val	Gly	Lys	Pro	Asn	Val	
		275					280					285				
Gly	Lys	Ser	Ser	Leu	Leu	Asn	Lys	Phe	Ala	Gly	Glu	Thr	Arg	Ser	Val	
	290					295					300					
Val	Asp	Asn	Val	Ala	Gly	Thr	Thr	Val	Asp	Pro	Val	Asp	Ser	Leu	Ile	
305					310					315					320	
Gln	Leu	Asp	Gln	Lys	Leu	Trp	Lys	Phe	Val	Asp	Thr	Ala	Gly	Leu	Arg	
				325					330					335		
Lys	Lys	Val	Lys	Thr	Ala	Ser	Gly	His	Glu	Tyr	Tyr	Ala	Ser	Leu	Arg	
			340					345					350			
Thr	His	Gly	Ala	Ile	Asp	Ala	Ala	Glu	Leu	Cys	Val	Leu	Leu	Ile	Asp	
		355					360					365				
Ser	Ser	Glu	Pro	Ile	Thr	Glu	Gln	Asp	Gln	Arg	Val	Leu	Ala	Met	Ile	
	370					375					380					
Thr	Asp	Ala	Gly	Lys	Ala	Leu	Val	Ile	Ala	Phe	Asn	Lys	Trp	Asp	Leu	
385					390					395					400	
Met	Asp	Glu	Asp	Arg	Arg	Ile	Asp	Leu	Asp	Arg	Glu	Leu	Asp	Leu	Gln	
				405					410					415		
Leu	Ala	His	Val	Pro	Trp	Ala	Lys	Arg	Ile	Asn	Ile	Ser	Ala	Lys	Thr	
			420					425					430			
Gly	Arg	Ala	Leu	Gln	Arg	Leu	Glu	Pro	Ala	Met	Leu	Glu	Ala	Leu	Asp	
		435					440					445				
Asn	Trp	Asp	Arg	Arg	Ile	Ser	Thr	Gly	Gln	Leu	Asn	Thr	Trp	Leu	Arg	
	450					455					460					
Glu	Ala	Ile	Ala	Ala	Asn	Pro	Pro	Pro	Met	Arg	Gly	Gly	Arg	Leu	Pro	
465					470					475					480	

Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
 485 490 495
 Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
 500 505 510
 Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
 515 520 525
 Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
 530 535 540

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 <212> DNA
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<220>
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 <222> (1)..(363)
 <223> RXS00738

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 ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg 96
 Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
 20 25 30
 cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac 144
 Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
 35 40 45
 gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg 192
 Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
 50 55 60
 atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa 240
 Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65 70 75 80
 gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg 288
 Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
 85 90 95
 gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att 336
 Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
 100 105 110
 ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg 383
 Phe Gly Gln Glu Lys Glu Ser Glu Ala
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 ctg 386

<210> 318
 <211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
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 Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
 20 25 30
 Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
 35 40 45
 Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
 50 55 60
 Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65 70 75 80
 Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
 85 90 95
 Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
 100 105 110
 Phe Gly Gln Glu Lys Glu Ser Glu Ala
 115 120

<210> 319

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXS01082

<400> 319

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 Leu Thr Gln Trp Gly
 1 5
 aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163
 Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
 10 15 20
 gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211
 Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
 25 30 35
 gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259
 Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
 40 45 50
 ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307
 Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
 55 60 65

ggt cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355
 Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
 70 75 80 85
 acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403
 Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
 90 95 100
 gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451
 Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
 105 110 115
 atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499
 Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
 120 125 130
 atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547
 Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
 135 140 145
 ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595
 Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
 150 155 160 165
 gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643
 Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
 170 175 180
 ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg 691
 Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu
 185 190 195
 cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca 739
 Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
 200 205 210
 aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct 783
 Asn Ala Val Arg Val Ser Arg
 215 220

<210> 320

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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 Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
 20 25 30
 Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
 35 40 45
 Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
 50 55 60
 Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg

65	70	75	80
Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala	85	90	95
His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro	100	105	110
Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp	115	120	125
Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn	130	135	140
Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val	145	150	155
Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly	165	170	175
Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser	180	185	190
Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile	195	200	205
Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg	210	215	220

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(547)
 <223> RXS01123

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 Met Arg Thr Leu Ala
 1 5
 gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg 163
 Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
 10 15 20
 cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
 Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
 25 30 35
 ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
 Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
 40 45 50
 gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
 Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu

55	60	65	
acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act			355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr			
70	75	80	85
tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag			403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys			
	90	95	100
ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc			451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile			
	105	110	115
gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg			499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val			
	120	125	130
tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc			547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly			
	135	140	145
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<210> 322			
<211> 149			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 322			
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Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys			
	20	25	30
Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val			
	35	40	45
Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn			
	50	55	60
Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro			
	65	70	75
Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly			
	85	90	95
His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met			
	100	105	110
Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser			
	115	120	125
Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln			
	130	135	140
Val Phe Asp Gln Gly			
145			

gca gcg cac ctc gcg ccg gga acc acc cgc aac tat tta tcc caa gct 643
Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn Tyr Leu Ser Gln Ala
170 175 180

atg aca aaa gta ggc gcg cag aat cgc ttt gaa gcg ttc acg cgc gcc 691
 Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu Ala Phe Thr Arg Ala
 185 190 195

agg gaa ttg ggc tgg ttg tagcttgtgg cttatctcct att 732
 Arg Glu Leu Gly Trp Leu
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<210> 324
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 324
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 Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr
 20 25 30
 Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn
 35 40 45
 Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly
 50 55 60
 Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val
 65 70 75 80
 Leu Ile Val Thr Ser His Ala Arg Pro Arg Gln Leu Lys Arg Ala Leu
 85 90 95
 Ala Ala Gly Val Leu Gly Phe Leu Pro Lys Thr Ser Thr Ala Asp Glu
 100 105 110
 Phe Ala Thr Ala Ile Arg Thr Val His Ala Gly Arg Arg Tyr Ile Asp
 115 120 125
 Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr
 130 135 140
 Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala
 145 150 155 160
 Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn
 165 170 175
 Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu
 180 185 190
 Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu
 195 200

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> RXS01242

<400> 325

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gacatatatta gtaaattggc tttttgcttt aaggagtgc atg tac gca gag gag 115
Met Tyr Ala Glu Glu
1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
40 45 50

ggc ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
105 110 115

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739

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Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210
 tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225
 gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245
 gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
 250 255
 tgattcttac agtcactgca agt 900

<210> 326
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 326
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 20 25 30
 Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45
 Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60
 Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80
 Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
 85 90 95
 Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
 100 105 110
 Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
 115 120 125
 Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
 130 135 140
 Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
 145 150 155 160
 Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
 165 170 175
 Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
 180 185 190
 Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val

195	200	205
Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser		
210	215	220
Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala		
225	230	235
Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val		
245	250	255

Ile Ala Glu

<210> 327
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(730)
 <223> RXS01607

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tttccgccccg ttttccctat ccacaaaagg accaagataa gtg atc cgt att ctg 115
 Val Ile Arg Ile Leu
 1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163
 Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu
 10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211
 Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp
 25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
 Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
 40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307
 Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
 55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
 Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
 70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
 Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
 90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
 Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
 105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499

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Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
    120                      125                      130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
    135                      140                      145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
    150                      155                      160

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
    170                      175                      180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
    185                      190                      195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
    200                      205                      210

cgtgttggtgta acc 753

<210> 328
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 328
Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly
  1                      5                      10                      15

Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met
    20                      25                      30

Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val
    35                      40                      45

Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu
    50                      55                      60

Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn
    65                      70                      75                      80

Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val
    85                      90                      95

Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser
    100                      105                      110

Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu
    115                      120                      125

Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn
    130                      135                      140

Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu
    145                      150                      155                      160

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<211> 1017
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> RXS01674
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cggtagacgg tacttttcata tccacccata taatgttgat																
Met Asp Asn Gly Trp																115
1 5																
ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg																163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly																
10 15 20																
agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc																211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala																
25 30 35																
agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg																259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu																
40 45 50																
gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt																307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu																
55 60 65																
gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa																355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu																
70 75 80 85																
tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg																403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly																
90 95 100																
gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac																451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp																
105 110 115																
atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat																499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn																

120	125	130	
tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt			547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly			
135	140	145	
ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg			595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val			
150	155	160	165
caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct			643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala			
	170	175	180
aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg			691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu			
	185	190	195
ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta			739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu			
	200	205	210
ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat			787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn			
	215	220	225
gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt			835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu			
230	235	240	245
ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt			883
Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser			
	250	255	260
gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg			931
Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp			
	265	270	275
agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc			979
Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile			
	280	285	290
gca tcg aac cac atc tgattttgag ccctggctaa cgg			1017
Ala Ser Asn His Ile			
295			

<210> 330

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met	Asp	Asn	Gly	Trp	Pro	Asn	Leu	Gln	Thr	Leu	Ala	Leu	Phe	Val	Ala
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Ile	Val	Glu	Glu	Gly	Ser	Leu	Gly	Ala	Gly	Ala	Arg	Lys	Val	Gly	Met
		20						25					30		

Ala	Gln	Pro	Asn	Ala	Ser	Arg	Ala	Ile	Ala	Glu	Leu	Glu	Ala	Asp	Met
		35					40					45			

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60
 Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80
 Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95
 Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110
 Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125
 Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140
 His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160
 His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175
 Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190
 Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
 195 200 205
 Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
 210 215 220
 Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
 225 230 235 240
 Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
 245 250 255
 Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
 260 265 270
 Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
 275 280 285
 Glu Leu Val Ser Ile Ala Ser Asn His Ile
 290 295

<210> 331

<211> 928

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXS01872

<400> 331

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attgcttggc tcatggagtt catcatgcgc caacagcaaa tattagtaaa atgtagaaa 60
tagctgtttt tgattcactt tgtgcatgta ggctgtgacc atg ggc aac gac ggc 115
                                         Met Gly Asn Asp Gly
                                         1                               5

gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
                               10                               15                               20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211
Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
                               25                               30                               35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
                               40                               45                               50

ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
                               55                               60                               65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
                               70                               75                               80                               85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
                               90                               95                               100

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451
Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
                               105                               110                               115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
                               120                               125                               130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac 547
Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
                               135                               140                               145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg 595
Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
                               150                               155                               160                               165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat 643
Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
                               170                               175                               180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act 691
His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
                               185                               190                               195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga 739
Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
                               200                               205                               210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg 787
Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
                               215                               220                               225

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gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca 835
 Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Gly Leu Val Ser Ala
 230 235 240 245

ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca 883
 Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr
 250 255 260

gtg gga atc gtg caa cgc cca ctt agt cca ccc gct tat agg gaa 928
 Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro Ala Tyr Arg Glu
 265 270 275

<210> 332

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
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 20 25 30

Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
 35 40 45

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
 50 55 60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
 65 70 75 80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
 85 90 95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
 100 105 110

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
 115 120 125

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
 130 135 140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
 145 150 155 160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
 165 170 175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
 180 185 190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
 195 200 205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
 210 215 220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala
225 230 235 240

Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp
245 250 255

Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro
260 265 270

Ala Tyr Arg Glu
275

<210> 333

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXS02117

<400> 333

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Val Ser Thr Asp Pro
1 5

gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc 163
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile
10 15 20

atc ctg ctc acc cggtat ggt gtc caa aac aca ccg acc aac aag cgc 211
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg
25 30 35

gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac 259
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp
40 45 50

gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt 307
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu
55 60 65

aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc 355
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly
70 75 80 85

tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt 403
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg
90 95 100

cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc 451
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg
105 110 115

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att 499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile

120 125 130
 aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa 547
 Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu
 135 140 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc tct 597
 Tyr Leu Asp Met Lys Trp Pro Arg Pro
 150 155

<210> 334
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 334
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 Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
 35 40 45
 Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
 50 55 60
 Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
 65 70 75 80
 Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
 85 90 95
 Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
 100 105 110
 Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp
 115 120 125
 Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn
 130 135 140
 Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro
 145 150 155

<210> 335
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(946)
 <223> RXS02288

<400> 335
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agtgctggat ctaacaacat ttccgtggta acctttttcac	atg tcc caa gtg att	115
	Met Ser Gln Val Ile	
	1 5	
ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc	163	
Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val		
	10 15 20	
acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag	211	
Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu		
	25 30 35	
gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259	
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp		
	40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307	
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser		
	55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355	
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val		
	70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403	
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala		
	90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451	
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys		
	105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499	
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr		
	120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547	
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile		
	135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595	
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys		
	150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643	
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val		
	170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691	
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His		
	185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739	
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly		
	200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787	
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly		
	215 220 225	

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
 230 235 240 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
 250 255 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
 265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa 969
 Thr Glu Glu Asp Phe
 280

<210> 336

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 336

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
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Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
 20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
 50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
 100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
 115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
 130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
 145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
 165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
 180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
 195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
 210 215 220
 Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
 225 230 235 240
 His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
 245 250 255
 Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
 260 265 270
 Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
 275 280

<210> 337
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(544)
 <223> RXS02573

<400> 337
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 gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc 115
 Met Thr Asn Lys Thr
 1 5
 atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163
 Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
 10 15 20
 tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg 211
 Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala
 25 30 35
 tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc 259
 Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr
 40 45 50
 ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc 307
 Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr
 55 60 65
 tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa gcg cga 355
 Cys Gln Glu Gly Val Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg
 70 75 80 85
 gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat 403
 Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp
 90 95 100
 gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg 451
 Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly
 105 110 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg 499
 Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val
 120 125 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac 544
 Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp
 135 140 145

taaaaccgag acgagaacca aga 567

<210> 338

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser
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Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val
 20 25 30

Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser
 35 40 45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser
 50 55 60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu
 65 70 75 80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp
 85 90 95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val
 100 105 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser
 115 120 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val
 130 135 140

Pro Pro Leu Asp
 145

<210> 339

<211> 866

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(843)

<223> RXS02627

<400> 339

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gga	gat	gct	gag	gct	gcg	ctg	gaa	ttc	ggt	gtg	cag	cct	gtg	ggt	gca	96
Gly	Asp	Ala	Glu 20	Ala	Ala	Leu	Glu	Phe 25	Gly	Val	Gln	Pro	Val 30	Gly	Ala	
tca	gat	tgg	ctc	gca	ttc	ggt	ggt	gaa	ggc	gtg	gga	ccg	tgg	att	gag	144
Ser	Asp	Trp 35	Leu	Ala	Phe	Gly	Gly 40	Glu	Gly	Val	Gly	Pro	Trp 45	Ile	Glu	
gat	tct	gcc	tac	gat	gaa	gcg	cca	gaa	ata	atc	gga	acc	atg	gaa	ccg	192
Asp	Ser	Ala	Tyr	Asp	Glu	Ala	Pro	Glu	Ile	Ile	Gly 60	Thr	Met	Glu	Pro	
50						55										
gag	tat	gaa	aag	att	gca	gcg	ctt	gaa	ccg	gat	ctg	att	ttg	gac	gtg	240
Glu	Tyr	Glu	Lys	Ile	Ala	Ala	Leu	Glu	Pro	Asp 75	Leu	Ile	Leu	Asp	Val 80	
65					70											
cgc	agc	tct	ggc	gac	cag	gaa	cgc	tat	gac	aag	ttg	tct	tca	atc	gca	288
Arg	Ser	Ser	Gly	Asp 85	Gln	Glu	Arg	Tyr	Asp 90	Lys	Leu	Ser	Ser	Ile	Ala	
ctg	acc	atc	ggc	gtt	cca	gaa	ggt	ggc	gat	agc	tac	ctc	acc	cca	cgc	336
Leu	Thr	Ile	Gly 100	Val	Pro	Glu	Gly	Gly 105	Asp	Ser	Tyr	Leu	Thr 110	Pro	Arg	
gct	gag	cag	gta	acc	atg	atc	gcc	act	gct	ctg	ggg	cag	gct	gaa	cgt	384
Ala	Glu	Gln	Val	Thr	Met	Ile	Ala	Thr	Ala	Leu	Gly	Gln	Ala	Glu	Arg	
115							120					125				
ggt	gaa	gaa	gtg	aac	gct	gaa	tac	gag	cag	ctc	act	gct	gat	att	cgt	432
Gly	Glu	Glu	Val	Asn	Ala	Glu	Tyr	Glu	Gln	Leu	Thr 140	Ala	Asp	Ile	Arg	
130						135										
gca	gct	cac	ccg	ggc	tgg	cct	gag	aag	acc	gcg	gct	gct	gta	tct	gca	480
Ala	Ala	His	Pro	Gly	Trp	Pro	Glu	Lys	Thr	Ala	Ala	Ala	Val	Ser	Ala	
145					150					155					160	
acg	gca	acc	agc	tgg	ggt	gca	tac	atc	aag	ggc	tcc	aac	cgt	gta	gat	528
Thr	Ala	Thr	Ser	Trp 165	Gly	Ala	Tyr	Ile	Lys 170	Gly	Ser	Asn	Arg	Val 175	Asp	
act	ttg	ctg	gac	ctg	ggc	ttc	cag	gaa	aac	cct	gag	ctg	gct	aaa	cag	576
Thr	Leu	Leu	Asp 180	Leu	Gly	Phe	Gln	Glu	Asn	Pro	Glu	Leu	Ala 190	Lys	Gln	
185																
caa	cct	ggc	gat	acg	ggt	ttc	tcc	atc	aaa	ttc	agt	gaa	gag	act	ttc	624
Gln	Pro	Gly	Asp	Thr	Gly	Phe	Ser	Ile	Lys	Phe	Ser	Glu	Glu	Thr	Phe	
195							200					205				
ggc	gtt	gtg	gat	tcc	gac	ctg	gtt	gtc	ggc	ttt	gcc	atc	ggt	atg	act	672
Gly	Val	Val	Asp	Ser	Asp	Leu	Val	Val	Gly	Phe	Ala 220	Ile	Gly	Met	Thr	
210						215										
cct	gag	gaa	atg	gca	gag	cag	gtt	cca	tgg	cag	atg	ttg	acc	gcc	act	720
Pro	Glu	Glu	Met	Ala	Glu	Gln	Val	Pro	Trp	Gln	Met	Leu	Thr	Ala	Thr	
225					230					235					240	
cgt	gac	ggc	cgt	tcc	ttt	gtg	atg	ccc	cgt	gag	att	tcc	aat	gcg	ttt	768
Arg	Asp	Gly	Arg	Ser	Phe	Val	Met	Pro	Arg	Glu	Ile	Ser	Asn	Ala	Phe	

245	250	255	
tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg			816
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val			
260	265	270	
cca ctt ctg gag gag cat gca ggg gag tagtggtccg gtggtgcggg cag			866
Pro Leu Leu Glu Glu His Ala Gly Glu			
275	280		

<210> 340

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp			
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Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala			
20	25	30	
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu			
35	40	45	
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro			
50	55	60	
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val			
65	70	75	80
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala			
85	90	95	
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg			
100	105	110	
Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg			
115	120	125	
Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg			
130	135	140	
Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala			
145	150	155	160
Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp			
165	170	175	
Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln			
180	185	190	
Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe			
195	200	205	
Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr			
210	215	220	
Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr			

225		230		235		240
Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe						
		245		250		255
Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val						
		260		265		270
Pro Leu Leu Glu Glu His Ala Gly Glu						
		275		280		

<210> 341
 <211> 930
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(907)
 <223> RXS02691

<400> 341
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 caccaaaaacc acacccttg ttagtaccag atcggctaaa atg aac acc atg cct 115
 Met Asn Thr Met Pro
 1 5
 gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163
 Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
 10 15 20
 gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211
 Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
 25 30 35
 aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259
 Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
 40 45 50
 ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307
 Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
 55 60 65
 tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc 355
 Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
 70 75 80 85
 gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403
 Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
 90 95 100
 cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451
 His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
 105 110 115
 atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499
 Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
 120 125 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547
 Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
 135 140 145
 gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595
 Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
 150 155 160 165
 ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643
 Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
 170 175 180
 ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691
 Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
 185 190 195
 gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739
 Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
 200 205 210
 gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787
 Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
 215 220 225
 cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835
 Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
 230 235 240 245
 gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883
 Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
 250 255 260
 ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc 930
 Leu Val Thr Arg Ser Glu Asp Leu
 265

<210> 342

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Asn Thr Met Pro Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr
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 Ala Ser Lys Gly Val Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val
 20 25 30
 Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu
 35 40 45
 Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
 50 55 60
 Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
 65 70 75 80
 Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
 85 90 95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
 100 105 110
 Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
 115 120 125
 Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
 130 135 140
 Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
 145 150 155 160
 Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
 165 170 175
 Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
 180 185 190
 Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
 195 200 205
 Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
 210 215 220
 Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
 225 230 235 240
 Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg
 245 250 255
 Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu
 260 265

<210> 343
 <211> 1161
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1138)
 <223> RXS02730

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 Met Ala Thr Glu Lys
 1 5
 ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
 Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
 10 15 20
 gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
 Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
 25 30 35
 act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
 Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala

40										45										50										
aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt	307																													
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly																														
55 60 65																														
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act	355																													
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr																														
70 75 80 85																														
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc	403																													
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr																														
90 95 100																														
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc	451																													
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu																														
105 110 115																														
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc	499																													
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys																														
120 125 130																														
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg	547																													
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu																														
135 140 145																														
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct	595																													
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser																														
150 155 160 165																														
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac	643																													
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn																														
170 175 180																														
aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca	691																													
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr																														
185 190 195																														
ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa	739																													
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys																														
200 205 210																														
att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga	787																													
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly																														
215 220 225																														
ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt	835																													
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe																														
230 235 240 245																														
gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag	883																													
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys																														
250 255 260																														
gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca	931																													
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr																														
265 270 275																														
cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa	979																													
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln																														
280 285 290																														

aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta 1027
 Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
 295 300 305

att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
 310 315 320 325

ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
 330 335 340

gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161
 Gly Leu Pro Asn Glu
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<210> 344

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
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Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
 20 25 30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
 35 40 45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
 50 55 60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65 70 75 80

Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
 85 90 95

Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
 100 105 110

Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
 115 120 125

Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
 130 135 140

Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
 145 150 155 160

Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
 165 170 175

Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
 180 185 190

Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala

195					200					205					
Cys	Ala	Asn	Ser	Lys	Ile	Gly	Glu	Gln	Leu	Val	Phe	Leu	Gly	Gly	Tyr
210						215					220				
Glu	Gln	Ser	Val	Gly	Phe	Glu	Gly	Ala	Thr	Lys	Leu	Leu	Asp	Gln	Gly
225					230					235					240
Ala	Lys	Thr	Leu	Phe	Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Val	Ile
				245					250					255	
Glu	Ala	Cys	His	Lys	Ala	Gly	Leu	Val	Ile	Gly	Lys	Asp	Val	Ser	Val
			260					265					270		
Ile	Gly	Phe	Asp	Thr	His	Pro	Leu	Phe	Ala	Leu	Gln	Pro	His	Pro	Leu
		275					280					285			
Thr	Val	Ile	Asp	Gln	Asn	Val	Glu	Gln	Leu	Ala	Gln	Arg	Ala	Val	Ser
						295					300				
Ile	Leu	Thr	Glu	Leu	Ile	Ala	Gly	Thr	Val	Pro	Ser	Val	Thr	Lys	Thr
305						310					315				320
Thr	Ile	Pro	Thr	Ala	Leu	Ile	His	Arg	Glu	Ser	Ile	Ile	Asn	Ser	Thr
				325					330					335	
Leu	Arg	Lys	Lys	Asp	Gly	Leu	Pro	Asn	Glu						
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<210> 345

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXS02818

<400> 345

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Ser	Tyr	Ser	Arg	Lys	Phe	Leu	Thr	Gln	Val	Trp	Ile	Arg	Asp	Asn	Val	
1				5					10					15		
ggc	gat	tat	aaa	ggc	ctt	acc	gat	acg	gcg	ttc	cgt	aag	aag	ctg	cag	96
Gly	Asp	Tyr	Lys	Gly	Leu	Thr	Asp	Thr	Ala	Phe	Arg	Lys	Lys	Leu	Gln	
			20					25					30			
cgc	gat	ctt	gcc	tac	ctg	cgc	aga	ggt	ggc	ggt	ccg	att	gag	cag	ttc	144
Arg	Asp	Leu	Ala	Tyr	Leu	Arg	Arg	Val	Gly	Val	Pro	Ile	Glu	Gln	Phe	
			35				40					45				
acg	gtc	acc	tca	ggc	ata	gct	gaa	ggc	cag	cag	gcg	tac	cgt	ctg	gcc	192
Thr	Val	Thr	Ser	Gly	Ile	Ala	Glu	Gly	Gln	Gln	Ala	Tyr	Arg	Leu	Ala	
			50			55					60					
cag	gat	tct	tat	aag	ctc	ccc	gag	gtc	gaa	ttc	acc	cca	gat	gag	gcc	240
Gln	Asp	Ser	Tyr	Lys	Leu	Pro	Glu	Val	Glu	Phe	Thr	Pro	Asp	Glu	Ala	
65					70					75					80	

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gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc 288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
      85                      90                      95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag 336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
      100                      105                      110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt 384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
      115                      120                      125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg 432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
      130                      135                      140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc 480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
      145                      150                      155                      160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc 528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
      165                      170                      175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc 576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
      180                      185                      190

cgc atc acc cgc gtc cgc aac atc aaa ctc 606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
      195                      200

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<210> 346

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
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Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
      20              25              30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
      35              40              45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
      50              55              60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
      65              70              75              80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
      85              90              95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
      100              105              110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly

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115		120		125
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu				
130		135		140
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro				
145		150		155
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg				
	165		170	175
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe				
	180		185	190
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu				
	195		200	

<210> 347

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(559)

<223> RXS02911

<400> 347

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agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa	115
Met Arg Thr Ser Lys	
1 5	

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc	163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser	
10 15 20	

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc	211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser	
25 30 35	

aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta	259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu	
40 45 50	

ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac	307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp	
55 60 65	

ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg	355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val	
70 75 80 85	

gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg	403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met	
90 95 100	

gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat	451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn	

105	110	115	
cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa			499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys			
120	125	130	
cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca			547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala			
135	140	145	
cga tta cat tca tgatgatgtc ctcagcaagt cca			582
Arg Leu His Ser			
150			

<210> 348
 <211> 153
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 348
 Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr
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 Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
 20 25 30
 Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
 35 40 45
 His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
 50 55 60
 Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
 65 70 75 80
 Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
 85 90 95
 Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala
 100 105 110
 Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu
 115 120 125
 Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg
 130 135 140
 Trp Pro Leu Arg Ala Arg Leu His Ser
 145 150

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 <211> 786
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(763)
 <223> RXS03066

<400> 349

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cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa 115
                                         Met Thr Ser Asp Lys
                                         1           5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
                        10                        15                        20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
                        25                        30                        35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
                        40                        45                        50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
                        55                        60                        65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
                        70                        75                        80                        85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                        90                        95                        100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
                        105                        110                        115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
                        120                        125                        130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
                        135                        140                        145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
                        150                        155                        160                        165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                        170                        175                        180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
                        185                        190                        195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct 739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
                        200                        205                        210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg 786

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Tyr Leu Phe Ser Val Ala Thr Gly
 215 220

<210> 350
 <211> 221
 <212> PRT
 <213> Corynebacterium glutamicum

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 Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
 20 25 30
 Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
 35 40 45
 Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
 50 55 60
 Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65 70 75 80
 Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
 85 90 95
 Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
 100 105 110
 Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
 115 120 125
 Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
 130 135 140
 Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
 145 150 155 160
 Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
 165 170 175
 Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
 180 185 190
 Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
 195 200 205
 Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
 210 215 220

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 <211> 565
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(565)

<223> RXS03208

<400> 351

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gcataaattg agtttggaag aacaaggaag gcagcctcct gtg aag gat ctg gtc 115
 Val Lys Asp Leu Val
 1 5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag 163
 Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu
 10 15 20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc 211
 Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser
 25 30 35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt 259
 Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu
 40 45 50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt 307
 Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg
 55 60 65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc 355
 Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu
 70 75 80 85

ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca 403
 Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala
 90 95 100

tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt 451
 Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val
 105 110 115

gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct 499
 Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro
 120 125 130

ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc 547
 Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly
 135 140 145

gtt cgt gcc atc gat ctg 565
 Val Arg Ala Ile Asp Leu
 150 155

<210> 352

<211> 155

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 352

Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr
 1 5 10 15

Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu
 20 25 30

Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met
 35 40 45
 Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met
 50 55 60
 Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg
 65 70 75 80
 Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys
 85 90 95
 Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val
 100 105 110
 Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe
 115 120 125
 Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp
 130 135 140
 Glu Pro Asp Ser Gly Val Arg Ala Ile Asp Leu
 145 150 155

<210> 353

<211> 562

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA00307

<400> 353

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gcataaattg agtttggaag aacaaggaag gcagcctcct gtg aag gat ctg gtc 115
 Val Lys Asp Leu Val
 1 5

gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag 163
 Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu
 10 15 20

ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc 211
 Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser
 25 30 35

ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt 259
 Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu
 40 45 50

gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt 307
 Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg
 55 60 65

tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc 355
 Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu

70	75	80	85	
ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca				403
Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala				
	90	95	100	
tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt				451
Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val				
	105	110	115	
gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct				499
Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro				
	120	125	130	
ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc				547
Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly				
	135	140	145	
gtt cgt gcc atc gat				562
Val Arg Ala Ile Asp				
	150			
<210> 354				
<211> 154				
<212> PRT				
<213> Corynebacterium glutamicum				
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Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr				
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Glu Leu Glu Glu Glu Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu				
	20	25	30	
Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met				
	35	40	45	
Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met				
	50	55	60	
Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg				
	65	70	75	80
Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys				
	85	90	95	
Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val				
	100	105	110	
Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe				
	115	120	125	
Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp				
	130	135	140	
Glu Pro Asp Ser Gly Val Arg Ala Ile Asp				
	145	150		

<210> 355

<400> 355																
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cataattttt accccaacgc ataggcttaa cggtgtgaat																115
Val 1 Lys 5 Leu 10 Thr 15 Asp 20																
gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att																163
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile																
10 15 20																
tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc																211
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala																
25 30 35																
gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt																259
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu																
40 45 50																
agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc																307
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile																
55 60 65																
aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac																355
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp																
70 75 80 85																
aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa																403
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu																
90 95 100																
aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca																451
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala																
105 110 115																
gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc																499
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe																
120 125 130																
aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg																547
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val																
135 140 145																
acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg																595
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu																
150 155 160 165																
gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc																643
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu																
170 175 180																
aqc acc qcc cga qac cgc aaa qcc qqa ttc atc aac qcc ctc qaa acc																691

Ser	Thr	Ala	Arg	Asp	Arg	Lys	Ala	Gly	Phe	Ile	Asn	Ala	Leu	Glu	Thr		
			185					190					195				
gaa	gcc	aca	caa	cgc	gga	atc	cgc	gaa	gaa	cta	cga	ttc	cgg	gta	gtt	739	
Glu	Ala	Thr	Gln	Arg	Gly	Ile	Arg	Glu	Glu	Leu	Arg	Phe	Arg	Val	Val		
		200					205					210					
cac	tcc	cgc	tac	tcc	ccc	acc	ggc	ggg	tat	gaa	gca	ttc	gca	gaa	ttc	787	
His	Ser	Arg	Tyr	Ser	Pro	Thr	Gly	Gly	Tyr	Glu	Ala	Phe	Ala	Glu	Phe		
	215					220					225						
cgc	aat	gat	ctc	cct	caa	atc	gtg	gtg	ccc	ctg	agc	acg	caa	tta	act	835	
Arg	Asn	Asp	Leu	Pro	Gln	Ile	Val	Val	Pro	Leu	Ser	Thr	Gln	Leu	Thr		
230					235					240					245		
cta	gga	gtt	ctc	aaa	gca	acc	caa	gaa	aac	ggc	ata	aaa	ata	tcg	gat	883	
Leu	Gly	Val	Leu	Lys	Ala	Thr	Gln	Glu	Asn	Gly	Ile	Lys	Ile	Ser	Asp		
			250						255					260			
gac	ctg	tca	ctt	gct	tgt	tac	ggc	gtc	gcc	gaa	tgg	ctc	gca	gtg	tgg	931	
Asp	Leu	Ser	Leu	Ala	Cys	Tyr	Gly	Val	Ala	Glu	Trp	Leu	Ala	Val	Trp		
			265					270					275				
ggc	cct	ggc	atc	acc	gtt	ttc	gca	cca	gac	ctc	cca	gcc	atg	ggc	gcc	979	
Gly	Pro	Gly	Ile	Thr	Val	Phe	Ala	Pro	Asp	Leu	Pro	Ala	Met	Gly	Ala		
		280					285					290					
gca	gct	gcc	acg	cag	gtt	tta	acg	ott	ctc	gac	gcc	gcc	cca	ctc	ccc	1027	
Ala	Ala	Ala	Thr	Gln	Val	Leu	Thr	Leu	Leu	Asp	Ala	Ala	Pro	Leu	Pro		
		295				300					305						
gaa	aac	cac	tta	agc	att	ccg	ggg	cag	ctc	att	gtc	cgt	ggg	aca	act	1075	
Glu	Asn	His	Leu	Ser	Ile	Pro	Gly	Gln	Leu	Ile	Val	Arg	Gly	Thr	Thr		
310					315					320					325		
cca	aag	gtt	taa	agg	taga	ggc	gcaca	aat	aat	gaaa	aatt					1114	
Pro	Lys	Val															

<210> 356

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

Val	Lys	Leu	Thr	Asp	Ala	Ala	Arg	Glu	Ala	Gly	Val	Gly	Tyr	Gly	Thr		
1				5					10					15			
Ala	Ser	Arg	Ala	Ile	Ser	Gly	Arg	Gly	Ser	Val	Asp	Ala	Ala	Thr	Arg		
			20					25					30				
Asp	Lys	Val	Leu	Ala	Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Arg	Thr	Asn	Ala		
		35					40					45					
Met	Ala	Arg	Ala	Leu	Arg	Glu	Asn	Lys	Thr	Arg	Thr	Val	Gly	Leu	Ile		
	50					55					60						
Val	Pro	Gly	Ile	Ile	Asn	Lys	Phe	Tyr	Thr	Glu	Ser	Ala	Thr	Val	Leu		
	65				70					75					80		

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
 85 90 95
 Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
 100 105 110
 Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
 115 120 125
 Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
 130 135 140
 Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
 145 150 155 160
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
 165 170 175
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
 180 185 190
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
 195 200 205
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
 210 215 220
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
 225 230 235 240
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
 245 250 255
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
 260 265 270
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
 275 280 285
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp
 290 295 300
 Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile
 305 310 315 320
 Val Arg Gly Thr Thr Pro Lys Val
 325

<210> 357

<211> 1107

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1084)

<223> FRXA02763

<400> 357

cgtgttttaa tctagaagtt taaagggtga aaacagtcca ttacttaagc accaatctgc 60

cataattttt	accccaacgc	ataggcttaa	cggtgtgaat	gtg	aag	tta	act	gac	115
				Val	Lys	Leu	Thr	Asp	
				1				5	
gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att	163								
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile									
	10	15	20						
tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc	211								
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala									
	25	30	35						
gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt	259								
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu									
	40	45	50						
agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc	307								
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile									
	55	60	65						
aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac	355								
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp									
	70	75	80	85					
aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa	403								
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu									
	90	95	100						
aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca	451								
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala									
	105	110	115						
gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc	499								
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe									
	120	125	130						
aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg	547								
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val									
	135	140	145						
acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg	595								
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu									
	150	155	160	165					
gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc	643								
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu									
	170	175	180						
agc acc gcc cga gac cgc aaa gcc gga ttc atc aac gcc ctc gaa acc	691								
Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile Asn Ala Leu Glu Thr									
	185	190	195						
gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt	739								
Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu Arg Phe Arg Val Val									
	200	205	210						
cac tcc cgc tac tcc ccc acc ggc ggt tat gaa gca ttc gca gaa ttc	787								
His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu Ala Phe Ala Glu Phe									
	215	220	225						

cgc aat gat ctc cct caa atc gtg gtg ccc ctg agc acg caa tta act 835
 Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu Ser Thr Gln Leu Thr
 230 235 240 245

cta gga gtt ctc aaa gca acc caa gaa aac ggc ata aaa ata tcg gat 883
 Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly Ile Lys Ile Ser Asp
 250 255 260

gac ctg tca ctt gct tgt tac ggc gtc gcc gaa tgg ctc gca gtg tgg 931
 Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu Trp Leu Ala Val Trp
 265 270 275

ggc cct ggc atc acc gtt ttc gca cca gac ctc cca gcc atg ggc gcc 979
 Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu Pro Ala Met Gly Ala
 280 285 290

gca gct gcc acg cag gtt tta acg ctt ctc gac gcc gcc cca ctc ccc 1027
 Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp Ala Ala Pro Leu Pro
 295 300 305

gaa aac cac tta agc att ccg ggg cag ctc att gtg cgt ggg aca act 1075
 Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile Val Arg Gly Thr Thr
 310 315 320 325

cca aag gtt taaaggtaga ggcgacacaat aat 1107
 Pro Lys Val

<210> 358

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Val Lys Leu Thr Asp Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr
 1 5 10 15

Ala Ser Arg Ala Ile Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg
 20 25 30

Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala
 35 40 45

Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile
 50 55 60

Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu
 65 70 75 80

Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
 85 90 95

Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
 100 105 110

Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
 115 120 125

Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
 130 135 140

Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
 145 150 155 160
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
 165 170 175
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
 180 185 190
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
 195 200 205
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
 210 215 220
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
 225 230 235 240
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
 245 250 255
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
 260 265 270
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
 275 280 285
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp
 290 295 300
 Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile
 305 310 315 320
 Val Arg Gly Thr Thr Pro Lys Val
 325

<210> 359
 <211> 759
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(759)
 <223> RXS03200

<400> 359
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 Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser
 1 5 10 15
 ttc ctc tcc cac gcc aag ggc gcc aac ggt tcg ctc act gga ccg ttg 96
 Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu
 20 25 30
 acc gta ggc atc atc ccc acg gcg gct cct tac att ttg ccg tca atg 144
 Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met
 35 40 45

ctg tcc atc gtg gat gaa gaa tat cca gat ctg gaa cct cac atc gtc 192
 Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val
 50 55 60

gag gac caa acc aag cat ctt ctc gcg ttg ctg cgc gac ggc gcc atc 240
 Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile
 65 70 75 80

gac gtc gcc atg atg gcc ctg cct tct gag gca cca ggc atg aag gaa 288
 Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu
 85 90 95

atc ccc ctc tac gac gaa gac ttt atc gtc gtt aca gct agc gat cac 336
 Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His
 100 105 110

ccc ttc gcc ggc cgc caa gac tta gaa cta tcc gcc tta gaa gac ctc 384
 Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu
 115 120 125

gat ctg ctg ctt ctc gac gac gga cac tgc ctc cac gac caa att gtg 432
 Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val
 130 135 140

gac ctg tgc cgc cgc gga gac atc aac ccc att agc tcc act act gct 480
 Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala
 145 150 155 160

gtc acc cgc gca tcc agc ctt acc acc gtc atg cag ctc gtc gtc gcc 528
 Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala
 165 170 175

ggc ctt gga tcc acc ttg gtc cca atc agc gca atc cca tgg gaa tgc 576
 Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys
 180 185 190

acc cga cca gga ctg gca aca gcc aac ttc aac tct gat gtc acc gca 624
 Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala
 195 200 205

aac cgc cgc att gga ttg gtg tac cgt tcc tct tct tct cgc gcc gaa 672
 Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
 210 215 220

gag ttc gaa cag ttt gca ctc att ttg cag cgc gct ttc caa gaa gcc 720
 Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
 225 230 235 240

gtc gcg ctt gct gcc tca act ggc atc acc ttg aag caa 759
 Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
 245 250

<210> 360

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser
 1 5 10 15

Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu
 20 25 30
 Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met
 35 40 45
 Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val
 50 55 60
 Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile
 65 70 75 80
 Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu
 85 90 95
 Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His
 100 105 110
 Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu
 115 120 125
 Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val
 130 135 140
 Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala
 145 150 155 160
 Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala
 165 170 175
 Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys
 180 185 190
 Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala
 195 200 205
 Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
 210 215 220
 Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
 225 230 235 240
 Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
 245 250

<210> 361

<211> 18

<212> DNA

• <213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Primer

<400> 361

ggaaacagta tgaccatg

<210> 362

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Primer

<400> 362

gtaaaacgac ggccagt